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(54) EXPRESSION OF RECOMBINANT FUSION PROTEINS IN ATTENUATED BACTERIA

EXPRESSION REKOMBINANTER FUSIONSPROTEINE IN ATTENUIERTEN BAKTERIEN

EXPRESSION DE PROTEINES RECOMBINANTES FUSIONNEES DANS DES BACTERIES
ATTENUEES

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Description

This invention relates to vaccine compositions containing attenuated bacteria.

In recent years, there has emerged a new generation of live oral salmonella vaccines based upon strains of Salmonella which have been attenuated by the introduction of a non-reverting mutation in a gene in the aromatic biosynthetic pathway of the bacterium. Such strains are disclosed, for example, in EP-A-0322237. The aforesaid live oral salmonella vaccines are showing promise as vaccines for salmonellosis in man and animals, and they can also be used effectively as carriers for the delivery of heterologous antigens to the immune system. Combined salmonella vaccines have been used to deliver antigens from viruses, bacteria, and parasites, eliciting secretory, humoral and cell-mediated immune responses to the recombinant antigens. Combined salmonella vaccines show great potential as single dose oral multivaccine delivery systems [C. Hormaeche *et al*, FEMS Symposium No. 63, Plenum, New York; pp 71-83, 1992].

There are problems to be overcome in the development of combined salmonella vaccines. A major consideration is obtaining a high level of expression of the recombinant antigen in the salmonella vaccine so that it will be sufficient to trigger an immune response. However, unregulated high level expression of foreign antigens can be toxic and affect cell viability [I. Charles and G. Dougan, TIBTECH 8, pp 117-21, 1990], rendering the vaccine ineffective or causing loss of the recombinant DNA. Several possible solutions to this problem have been described, such as expression from plasmids carrying essential genes, "on-off" promoters or incorporation of the foreign genes into the salmonella chromosome.

An alternative approach to overcoming the aforesaid problem would be to use a promoter which is inducible *in vivo*, and one such promoter is the E. coli nitrite reductase promoter nirB which is induced under anaerobiosis and has been used in biotechnology for the production of tetanus toxin fragment C (TetC) of Clostridium tetani [M.D. Oxe *et al*/Nucl. Ac. Res., 19, pp 2889-92, 1991]. It has previously been found by the inventors of this application (S.N. Chatfield *et al* Bio/Technology, Vol. 10, pp 888-92 1992) that an Aro Salmonella harbouring a construct expressing TetC from the nirB promoter (pTETnir15) elicited very high anti-tetanus antibody responses in mice. The article by Chatfield *et al* was published after the priority date of this application.

However, we have also found that when it was attempted to express the P28 antigen from Schistosoma mansoni alone from nirB, the resulting construct was not immunogenic.

Tetanus toxoid has been extensively used as an adjuvant for chemically coupled guest epitopes [D.A. Herrington *et al*. Nature, 328, pp 257-9 1987]. The potent immunogenicity of TetC in Salmonella suggested to us that it may be possible to exploit this character to promote the immune response of the guest peptides or proteins. However, fusing two proteins together often leads to an incorrectly folded chimaeric protein which no longer retains the properties of the individual components. For example the B subunit of the Vibrio cholerae (CT-B) and E. coli (LT-B) enterotoxins are powerful mucosal immunogens but genetic fusions to these subunits can alter the structure and properties of the carrier and hence their immunogenicity [see M. Sandkvist *et al*. J. Bacteriol 169, pp 4570-6, 1987, Clements 1990 and M. Lipscombe *et al* [Mol. Microbiol 5, pp 1385 1990]. Moreover, many heterologous genes expressed in bacteria are not produced in soluble properly folded, or active forms and tend to accumulate as insoluble aggregates [see C. Schein *et al*. Bio/Technology 6, pp 291-4, 1988 and R. Halenbeck *et al*; Bio/Technology 7, pp 710-5, 1989].

It is an object of the invention to overcome the aforementioned problems.

We have now found that efficient expression of recombinant antigens, and in particular fusion proteins, can be achieved in bacteria such as salmonellae, by the use of an inducible promoter such as nirB and by incorporating a flexible hinge region between two antigenic components of the fusion protein. The resulting recombinant antigens have been shown to have good immunogenicity. It has also been found, surprisingly, that enhanced expression of a protein can be obtained when a gene coding for the protein is linked to the gene for tetanus toxin C fragment.

Accordingly, in a first aspect, the present invention provides a vaccine composition comprising a pharmaceutically acceptable carrier and an attenuated bacterium containing a DNA construct comprising a promoter which is capable of promoting expression of a sequence under, and has activity which is induced under, anaerobic conditions, the promoter being operably linked to a DNA sequence encoding first and second proteins linked by a chain of amino acids defining a hinge region.

A preferred promoter is the nirB promoter or a part or derivative thereof which is capable of promoting expression of a sequence under anaerobic conditions.

Other particular and preferred aspects of the invention are as defined in the dependent claims appended hereto.

The first and second proteins are preferably heterologous proteins and in particular can be polypeptide immunogens; for example they may be antigenic sequences derived from a virus, bacterium, fungus, yeast or parasite. In particular, it is preferred that the first said protein is an antigenic sequence comprising tetanus toxin fragment C or epitopes thereof.

The second protein is preferably an antigenic determinant of a pathogenic organism. For example, the antigenic determinant may be an antigenic sequence derived from a virus, bacterium, fungus, yeast or parasite.

Examples of viral antigenic sequences for the first and/or second heterologous proteins are sequences derived from a type of human immuno-deficiency virus (HIV) such as HIV-1 or HIV-2, the CD4 receptor binding site from HIV, for example from HIV-1 or -2, hepatitis A or B virus, human rhinovirus such as type 2 or type 14, Herpes simplex virus, poliovirus type 2 or 3, foot-and-mouth disease virus (FMDV), rabies virus, rotavirus, influenza virus, coxsackie virus, human papilloma virus (HPV), for example the type 16 papilloma virus, the E7 protein thereof, and fragments containing the E7 protein or its epitopes; and simian immunodeficiency virus (SIV). Examples of antigens derived from bacteria are those derived from Bordetella pertussis (e.g. P69 protein and filamentous haemagglutinin (FHA) antigens), Vibrio cholerae, Bacillus anthracis, and E.coli antigens such as E.coli heat Labile toxin B subunit (LT-B), E.coli K88 antigens, and enterotoxigenic E.coli antigens. Other examples of antigens include the cell surface antigen CD4, Schistosoma mansoni P28 glutathione S-transferase antigens (P28 antigens) and antigens of flukes, mycoplasma, roundworms, tapeworms, Chlamydia trachomatis, and malaria parasites, eg. parasites of the genus plasmodium or babesia, for example Plasmodium falciparum, and peptides encoding immunogenic epitopes from the aforementioned antigens.

Particular antigens include the full length Schistosoma mansoni P28, and oligomers (e.g. 2, 4 and 8-mers) of the immunogenic P28 aa 115-131 peptide (which contains both a B and T cell epitope), and human papilloma virus E7 protein, Herpes simplex antigens, foot and mouth disease virus antigens and simian immunodeficiency virus antigens.

The promoter sequence has activity which is induced in response to a change in the surrounding environment, i.e. is induced by anaerobic conditions. A particular example of such a promoter sequence is the nirB promoter which has been described, for example in International Patent Application WO-A-92/15689. The nirB promoter has been isolated from E.coli, where it directs expression of an operon which includes the nitrite reductase gene nirB (Jayaraman *et al*, J. Mol. Biol. 196, 781-788, 1987), and nirD, nirC, cysG (Peakman *et al*, Eur. J. Biochem. 191, 315-323, 1990). It is regulated both by nitrite and by changes in the oxygen tension of the environment, becoming active when deprived of oxygen, (Cole, Biochem. Biophys. Acta. 162, 356-368, 1968). Response to anaerobiosis is mediated through the protein FNR, acting as a transcriptional activator, in a mechanism common to many anaerobic respiratory genes. By deletion and mutational analysis the part of the promoter which responds solely to anaerobiosis has been isolated and by comparison with other anaerobically-regulated promoters a consensus FNR-binding site has been identified (Bell *et al*, Nucl. Acids. Res. 17, 3865-3874, 1989; Jayaraman *et al*, Nucl. Acids. Res. 17, 135-145, 1989). It has also been shown that the distance between the putative FNR-binding site and the -10 homology region is critical (Bell *et al*, Molec. Microbiol. 4, 1753-1763, 1990). It is therefore preferred to use only that part of the nirB promoter which responds solely to anaerobiosis. As used herein, references to the nirB promoter refer to the promoter itself or a part or derivative thereof which is capable of promoting expression of a coding sequence under anaerobic conditions. The preferred sequence, and which contains the nirB promoter is: AATTCAGGTAAATTTGATGTACATCAAAATGGTACCCCTTGCTGAATCGTTAAGG TAGGCGGTAGGGCC (SEQ ID NO: 1)

The hinge region is a region designed to promote the independent folding of both the first and second proteins by providing both spatial and temporal separation between the domains.

The hinge region typically is a sequence encoding a high proportion of proline and/or glycine amino acids. The hinge region may be composed entirely of proline and/or glycine amino acids. The hinge region may comprise one or more glycine-proline dipeptide units.

The hinge region may, for example, contain up to about fifteen amino acids, for example at least 4 and preferably 6-14 amino acids, the number of amino acids being such as to impart flexibility between the first and second proteins.

In one embodiment, the hinge region can correspond substantially to the hinge domain of an antibody immunoglobulin. The hinge regions of IgG antibodies in particular are rich in prolines [T.E. Michaelson *et al*. J. Biol. Chem. 252, 883-9 1977], which are thought to provide a flexible joint between the antigen binding and tail domains.

Without wishing to be bound by any theory, the prolines are thought to form the rigid part of the hinge as the ring structure characteristic of this amino acid hinders rotation around the peptide bond that connects the proline residue with an adjacent amino acid. This property is thought to prevent proline, and adjacent residues, from adopting the ordered structure of an alpha helix or beta strand. Flexibility is thought to be imparted by glycine, the simplest amino acid, with very limited steric demands. Glycine is thought to function as a flexible elbow in the hinge. Other amino acids may be substituted for glycine, particularly those without bulky side-chains, such as alanine, serine, asparagine and threonine.

In one preferred embodiment, the hinge region is a chain of four or more amino acids defining the sequence



wherein Pro is proline, X and Y are each glycine, or an amino acid having a non-bulky side chain; Z is any amino acid; p is a positive integer; q is a positive integer of from one to ten; and r is zero or a positive integer greater than zero.

The hinge region can be a discrete region heterologous to both the first and second proteins or can be defined by a carboxy-end portion of the first protein or an amino-end portion of the second protein.

Codons which are infrequently utilised in *E.coli* [H. Grosjean *et al*, Gene 18, 199-209, 1982] and *Salmonella* are selected to encode for the hinge, as such rare codons are thought to cause ribosomal pausing during translation of the messenger RNA and allow for the correct folding of polypeptide domains [I.J. Purvis *et al*, J. Mol. Biol. 193, 413-7 1987]. In addition, where possible restriction enzymes are chosen for the cloning region which, when translated in the resulting fusion, do not encode for bulky or charged side-groups.

In a preferred embodiment of the invention, the *nirB* promoter sequence is operably linked to a DNA sequence encoding first and second polypeptide immunogens linked by a hinge region, wherein the first polypeptide immunogen comprises tetanus toxin fragment C or epitopes thereof.

It has been found that by providing a DNA sequence encoding tetanus toxin fragment C (TetC) linked via a hinge region to a second sequence encoding an antigen, the expression of the sequence in bacterial cells is enhanced relative to constructs wherein the fragment C and hinge region are absent. For example, the expression level of the full length P28 protein of *S. mansoni* when expressed as a fusion to TetC was greater than when the P28 protein was expressed alone from the *nirB* promoter. The TetC fusions to the full length P28 protein of *S. mansoni* and its tandem epitopes were all soluble and expressed in both *E.coli* and *S.typhimurium*. In addition, the TetC-P28 fusion protein was capable of being affinity purified by a glutathione agarose matrix, suggesting that the P28 had folded correctly to adopt a conformation still capable of binding to its natural substrate.

Stable expression of the first and second heterologous proteins linked by the hinge region can be obtained *in vivo*. The heterologous proteins can be expressed in an attenuated bacterium which can thus be used as a vaccine.

The attenuated bacterium may be selected from the genera *Salmonella*, *Bordetella*, *Vibrio*, *Haemophilus*, *Neisseria* and *Yersinia*. Alternatively, the attenuated bacterium may be an attenuated strain of enterotoxigenic *Escherichia coli*. In particular the following species can be mentioned: *S.typhi* - the cause of human typhoid; *S.typhimurium* - the cause of salmonellosis in several animal species; *S.enteritidis* - a cause of food poisoning in humans; *S.choleraesuis* - a cause of salmonellosis in pigs; *Bordetella pertussis* - the cause of whooping cough; *Haemophilus influenzae* - a cause of meningitis; *Neisseria gonorrhoeae* - the cause of gonorrhoea; and *Yersinia* - a cause of food poisoning.

Attenuation of the bacterium may be attributable to a non-reverting mutation in a gene in the aromatic amino acid biosynthetic pathway of the bacterium. There are at least ten genes involved in the synthesis of chorismate, the branch point compound in the aromatic amino acid biosynthetic pathway. Several of these map at widely differing locations on the bacterial genome, for example *aroA* (5-enolpyruvylshikimate-3-phosphate synthase), *aroC* (chorismate synthase), *aroD* (3-dihydroquinone dehydratase) and *aroE* (shikimate dehydrogenase). A mutation may therefore occur in the *aroA*, *aroC*, *aroD*, or *aroE* gene.

Preferably, however, an attenuated bacterium harbours a non-reverting mutation in each of two discrete genes in its aromatic amino acid biosynthetic pathway. Such bacteria are disclosed in EP-A-0322237. Double *aro* mutants which are suitable are *aroA aroC*, *aroA aroD*, and *aroA aroE*. Other bacteria having mutations in other combinations of the *aroA*, *aroC*, *aroD* and *aroE* genes are however useful. Particularly preferred are *Salmonella* double *aro* mutants, for example double *aro* mutants of *S.typhi* or *S.typhimurium*, in particular *aroA aroC*, *aroA aroD* and *aroA aroE* mutants. Alternatively, the attenuated bacterium may harbour a non-reverting mutation in a gene concerned with the regulation of one or more other genes (EP-A-0400958). Preferably the mutation occurs in the *ompR* gene or another gene involved in regulation. There are a large number of other genes which are concerned with regulation and are known to respond to environmental stimuli (Ronson *et al*, Cell 49, 579-581).

This type of attenuated bacterium may harbour a second mutation in a second gene. Preferably the second gene is a gene encoding for an enzyme involved in an essential biosynthetic pathway, in particular genes involved in the pre-chorismate pathway involved in the biosynthesis of aromatic compounds. The second mutation is therefore preferably in the *aroA*, *aroC* or *aroD* gene.

Another type of attenuated bacterium is one in which attenuation is brought about by the presence of a non-reverting mutation in DNA of the bacterium which encodes, or which regulates the expression of DNA encoding, a protein that is produced in response to environmental stress. Such bacteria are disclosed in WO 91/15572. The non-reverting mutation may be a deletion, insertion, inversion or substitution. A deletion mutation may be generated using a transposon.

The vaccine composition of the invention may comprise one or more suitable adjuvants.

The vaccine composition is advantageously presented in a lyophilised form, for example in a capsular form, for oral administration to a patient. Such capsules may be provided with an enteric coating comprising, for example, Eudragit "S", Eudragit "L", Cellulose acetate, Cellulose acetate phthalate or hydroxypropylmethyl Cellulose. These capsules may be used as such, or alternatively, the lyophilised material may be reconstituted prior to administration, e.g. as a suspension. Reconstitution is advantageously effected in buffer at a suitable pH to ensure the viability of the organisms. In order to protect the attenuated bacteria and the vaccine from gastric acidity, a sodium bicarbonate preparation is advantageously administered before each administration of the vaccine. Alternatively, the vaccine may be prepared for parenteral administration, intranasal administration or intramammary administration.

The vaccine composition of the invention may be used in the prophylactic treatment of a host, particularly a human

host but also possibly an animal host. An infection caused by a micro-organism, especially a pathogen, may therefore be prevented by administering an effective dose of an attenuated bacterium in a vaccine composition according to the invention. The bacterium then expresses a heterologous protein or proteins capable of raising antibody to the micro-organism. The dosage employed will be dependent on various factors including the size and weight of the host, the type of vaccine formulated and the nature of the heterologous protein.

An attenuated bacterium useful in a vaccine composition according to the present invention may be prepared by transforming an attenuated bacterium with a DNA construct as hereinbefore defined. Any suitable transformation technique may be employed, such as electroporation. In this way, an attenuated bacterium capable of expressing a protein or proteins heterologous to the bacterium may be obtained. A culture of the attenuated bacterium may be grown under aerobic conditions. A sufficient amount of the bacterium is thus prepared for formulation as a vaccine, with minimal expression of the heterologous protein occurring.

The DNA construct may be a replicable expression vector comprising the *nirB* promoter operably linked to a DNA sequence encoding the tetanus toxin C fragment or epitopes thereof and the second heterologous protein, linked by a hinge region. The *nirB* promoter may be inserted in an expression vector, which already incorporates a gene encoding one of the heterologous proteins (e.g. tetanus toxin C fragment), in place of the existing promoter controlling expression of the protein. The hinge region and gene encoding the second heterologous protein (e.g. an antigenic sequence) may then be inserted. The expression vector should, of course, be compatible with the attenuated bacterium into which the vector is to be inserted.

The expression vector is provided with appropriate transcriptional and translational control elements including, besides the *nirB* promoter, a transcriptional termination site and translational start and stop codons. An appropriate ribosome binding site is provided. The vector typically comprises an origin of replication and, if desired, a selectable marker gene such as an antibiotic resistance gene. The vector may be a plasmid.

The invention will now be illustrated but not limited, by reference to the following examples and the accompanying drawings, in which:

Figure 1 is a schematic illustration of the construction of an intermediate plasmid pTECH1 in accordance with one aspect of the invention.

Figure 2 is a schematic illustration of the construction of a second intermediate plasmid pTECH2.

Figure 3 is a schematic illustration of the construction of a plasmid of the invention using the intermediate plasmid of Figure 2 as the starting material. In Figure 3 B = *Bam*HI, E = *Eco*RV; H = *Hind*III; X = *Xba*I; S = *Spe*I.

Figure 4 is a schematic illustration of the construction of a plasmid containing repeating epitopes (repiteps).

Figure 5 illustrates antibody responses against recombinant *S. mansoni* protein P28 as detected by ELISA in mice inoculated intravenously with SL3261, SL3261(pTETnir15), SL3261 (pTECH2), SL3261(pTECH2-monomer), SL3261 (pTECH2-dimer), SL3261(pTECH2-tetramer), SL3261(pTECH2-octamer), and SL3261(pTECH1-P28). In Figure 5 the results are expressed as OD in individual mice at intervals after immunisation.

Figure 6 illustrates antibody responses against TetC as detected by ELISA in mice inoculated as in Figure 5.

Figure 7 illustrates antibody responses against peptide 115-131 of the P28 protein coupled to ovalbumin as detected by ELISA in mice inoculated intravenously with SL3261, SL3261(pTECH2), SL3261(pTECH2-monomer), SL3261(pTECH2-dimer), SL3261(pTECH2-tetramer), and

SL3261(pTECH2-octamer).

Figure 8 illustrates antibody responses against TetC as detected by ELISA from mice inoculated orally with SL3261 (pTECH1-P28).

Figure 9 illustrates antibody responses against recombinant P28 as detected by ELISA in mice inoculated as in Figure 8.

Figure 10 illustrates schematically the preparation of various constructs from the pTECH2 intermediate plasmid.

Figure 11 illustrates schematically the structure of tripartite protein structures ("heteromers") prepared using pTECH2.

Figure 12 shows the DNA sequence of the vector pTECH1. (SEQ ID NO: 17).

Figure 13 shows the DNA sequence of the vector pTECH2. (SEQ ID NO: 18).

Figure 14 illustrates, schemetically, the restriction sites on the vector pTECH2.

EXAMPLE 1

Preparation of pTECH1

The preparation of pTECH1, a plasmid incorporating the *nirB* promoter and TetC gene, and a DNA sequence

encoding a hinge region and containing restriction endonuclease sites to allow insertion of a gene coding for a second or guest protein, is illustrated in Figure 1. Expression plasmid pTETnir15, the starting material shown in Figure 1, was constructed from pTETtacII5 (Makoff *et al*, Nucl. Acids Res. 17 10191-10202, 1989); by replacing the EcoRI-ApaI region (1354bp) containing the lacI gene and tac promoter with the following pair of oligos 1 and 2:

Oligo-1 5' AATTCAGGTAAATTTGATGTACATCAAATGGTACCCCTTGCTGAAT

Oligo-2 3' -GTCCATTTAAACTACATGTAGTTTACCATGGGGAACGACTTA

CGTTAAGGTAGGCGGTAGGGCC-3' (SEQ ID NO: 2)

GCAATTCCATCCGCCATC-5' (SEQ ID NO: 3)

The oligonucleotides were synthesised on a Pharmacia Gene Assembler and the resulting plasmids confirmed by sequencing (Makoff *et al*, Bio/Technology 7, 1043-1046, 1989).

The pTETnir15 plasmid was then used for construction of the novel pTECH1 plasmid incorporating a polylinker region suitable as a site for insertion of heterologous DNA to direct the expression of fragment C fusion proteins. pTETnir15 is a known pAT153-based plasmid which directs the expression of fragment C. However, there are no naturally occurring convenient restriction sites present at the 3'-end of the TetC gene. Therefore, target sites, preceded by a hinge region, were introduced at the 3'-end of the TetC coding region by means of primers tailored with "add-on" adapter sequences (Table 1), using the polymerase chain reaction (PCR) [K. Mullis *et al*, Cold Spring Harbor Sym. Quant. Biol. 51, 263-273 1986]. Accordingly, pTETnir15 was used as a template in a PCR reaction using primers corresponding to regions covering the SacII and BamHI sites. The anti-sense primer in this amplification was tailored with a 38 base 5'-adaptor sequence. The anti-sense primer was designed so that a sequence encoding novel XbaI, SpeI and BamHI sites were incorporated into the PCR product. In addition, DNA sequences encoding additional extra amino acids including proline were incorporated (the hinge regions) and a translation stop codon signal in frame with the fragment C open reading frame.

The PCR product was gel-purified and digested with SacII and BamHI, and cloned into the residual 2.8 kb vector pTETnir15 which had previously been digested by SacII and BamHI. The resulting plasmid purified from transformed colonies and named pTECH 1 is shown in Figure 1. Heterologous sequences such as the sequence encoding the Schistosoma mansoni P28 glutathione S-transferase (P28) were cloned into the XbaI SpeI and BamHI sites in accordance with known methods.

EXAMPLE 2

Construction of pTECH2

To further improve the utility of pTECH1, a short linker sequence was introduced between the XbaI and BamHI sites in pTECH1 to allow the directional cloning of oligonucleotides and to also facilitate the construction of multiple tandem epitopes, ("reptopes") (Figure 2). Two complementary oligonucleotides were synthesised bearing the restriction enzyme target sites for BamHI, EcoRV, HindIII, SpeI, followed by a translational stop codon (Table 1). The oligonucleotides were tailored with XbaI and BamHI cohesive ends; however, the BamHI target sequence was designed to include a mismatch and, upon cloning, this restriction site in pTECH1 is destroyed. This version of the vector was designated pTECH2.

EXAMPLE 3

Construction of pTECH1-P28

A P28 gene expression cassette was produced by PCR using pUC19-P28 DNA (a kind gift from Dr R Pierce, Pasteur Institute, Lille) as template. Oligonucleotide primers were designed to amplify the full length P28 gene beginning

with the start codon and terminating with the stop codon. In addition, the sense and antisense primers were tailored with the restriction sites for XbaI and BamHI respectively. The product was gel-purified and digested with XbaI and BamHI and then cloned into pTECH1 which had previously been digested with these enzymes and subsequently gel-purified.

Expression of the TetC-P28 fusion protein

Expression of the TetC-P28 fusion protein was evaluated by SDS-PAGE and Western blotting of bacterial cells harbouring the construct. It was found that the fusion protein remains soluble, cross-reacts with antisera to both TetC and P28, and is also of the expected molecular weight, 80kDa, for a full length fusion.

The fusion protein was stably expressed in a number of different genetic backgrounds including E. coli (TG2) and S. typhimurium (SL5338, SL3261) as judged by SDS-PAGE and Western blotting. Of interest was a minor band of 50kDa which co-migrates with the TetC-Hinge protein alone and cross-reacts exclusively with the anti-TetC sera. As the codon selection in the hinge region has been designed to be suboptimal, the rare codons may cause pauses during translation which may occasionally lead to the premature termination of translation, thus accounting for this band.

Affinity purification of the TetC-P28 fusion

Glutathione is the natural substrate for P28, a glutathione S-transferase. The amino acid residues involved in binding glutathione are thought to be spatially separated in the primary structure of the polypeptide and brought together to form a glutathione binding pocket in the tertiary structure (P. Reinemer *et al.* EMBO, J8, 1997-2005, 1991). In order to gauge whether the P28 component of the fusion has folded correctly to adopt a conformation capable of binding glutathione, its ability to be affinity purified on a glutathione-agarose matrix was tested. The results obtained (not shown) demonstrated that TetC-P28 can indeed bind to the matrix and the binding is reversible, as the fusion can be competitively eluted with free glutathione.

EXAMPLE 4

Construction of pTECH2-P28(aa115-131) peptide fusions

Complementary oligonucleotides encoding the aa115-131 peptide were designed with a codon selection for optimal expression in E. coli [H. Grosjean *et al.* idem]. The oligonucleotides were tailored with BglII and SpeI cohesive ends which were generated upon annealing and cloned into pTECH2 which had previously been digested with BamHI and SpeI (Figure 3).

Repeated tandem copies of the epitopes (repeats) were constructed in pTECH2 by the following approach. The recombinant fusion vector was digested with XbaI and SpeI and to each digest was added a second restriction enzyme which cuts uniquely elsewhere within the vector, e.g. PstI which makes a cut exclusively within the ampicillin resistance gene (Figure 4). DNA fragments containing the epitope sequences can be purified from each of the double digests, mixed and then ligated. XbaI cleaves its target sequence to generate a 5'-CTAG overhang which is compatible with the SpeI overhang. Upon ligation the recognition sequences of both these enzymes are destroyed. In this way the XbaI-SpeI restriction sites remain unique and the procedure can be simply and effectively repeated to construct recombinant fusion vectors expressing four or eight tandem copies of the epitopes (Figure 4). A similar strategy has been used by others in the generation of a multimeric fusion protein for the production of a neuropeptide [T. Kempe *et al.* Gene 39, 239-45, 1985].

Expression of the TetC-peptide fusion proteins

Expression of the TetC-peptide fusions as monomeric, dimeric, tetrameric, and octameric tandem peptide repeats was evaluated by SDS-PAGE and Western blotting of the bacterial strains harbouring the constructs. The fusion proteins remain soluble, cross-react with both antisera to TetC and P28, and are also of the expected molecular weight [Figure 5]. Furthermore the fusion proteins are expressed in a number of different genetic backgrounds including E. coli (TG2) and S. typhimurium (SL5338, SL3261) as judged by SDS-PAGE and Western blotting. There appeared to be some degradation of the repeats consisting of higher numbers of copies, as indicated by the appearance of faint bands of lower molecular weight seen in Western blots probed with the anti-P28 antibody.

The size of the bands suggested that they consisted of reduced copy number fusions to TetC. As was the case with the TetC-P28 fusion described above, the level of expression of the TetC-peptide fusions was less than that of TetC alone from pTECH2, with the expression level gradually decreasing with increasing copy number.

EXAMPLE 5

Immunological Studies

Stability of the plasmid constructs in vivo and immunisation of mice

BALB/c mice were given approx. 10^6 cfu i/v or 5×10^9 orally of *S. typhimurium* SL3261 and SL3261 harbouring the different constructs. Viable counts on homogenates of liver, spleen and (for orally inoculated mice) lymph nodes performed from days 1-8 (epitope fusions) and 1-11 (vector, octamer and P28 fusions) were similar on media with and without ampicillin, indicating that the plasmids were not being lost during growth in the tissues.

Antibody responses in mice immunised intravenously Antibody responses to the TetC-P28 fusion

Tail bleeds were taken weekly on weeks 3 to 6 from animals from each group of 8 mice. Figure 5 shows that in mice immunised with salmonellae expressing the TetC-P28 fusion, antibody responses to recombinant P28 appeared by week 3, and were positive in 6/6 mice from week 4 onwards. No anti-P28 antibodies were detected in sera from mice immunised with either SL3261 or SL3261-pTETnir15 or pTECH2.

All mice immunised with salmonellae expressing TetC, either alone or as the TetC-P28 fusion (but not with salmonellae alone), made antibody to TetC appearing as early as the third week. (Figure 6).

Antibody responses to the TetC-peptide fusions

Mice immunised with salmonellae expressing TetC fused to multiple copies of the aa 115-131 peptide were bled as above and the sera tested by ELISA against the synthetic 115-131 peptide chemically conjugated to ovalbumin, and against recombinant P28. Figure 7 shows that antibody responses to the peptide were detected as early as week 3 and increased thereafter, with responses being stronger to fusions containing greater numbers of copies of the peptide. The octameric fusions elicited the best responses with 4-5 mice positive. No antibody responses were detected against ovalbumin-monomer or recombinant P28 in mice immunised either with SL3261, pTECH2 or the monomeric epitope fusion.

Some of the anti-epitope sera recognised the full length P28 protein in ELISA (Figure 5). One mouse injected with the dimeric fusion was positive at week 5, another mouse injected with the tetrameric fusion was positive at week 3. Thereafter sera from at least two mice injected with the octameric fusion consistently recognised P28 from week four up to week six.

In summary the antibody responses against the repitopes improved dramatically with increasing copy number, with the tetrameric and octameric repitope fusions being the most potent. No antibody responses to the monomeric fusion were detected.

Antibody response to TetC in mice immunised with the different fusions

The antibody response to TetC was not the same in all groups; the addition of C-terminal fusions to TetC clearly modified the response. Figure 6 shows that the antibody response to TetC elicited by the vector pTECH2 (TetC-Hinge alone) was significantly less than the TetC response to the parental vector, pTETnir15. Surprisingly, the addition to TetC of fusions of increasing size dramatically restores the response to TetC. The anti-TetC response to the largest fusion, full length P28 in pTECH1, was similar to the response to TetC obtained from the parental plasmid (under the conditions tested). Sera from mice injected with non-recombinant SL3261 did not react with TetC at any time during the period tested.

Antibody responses in mice immunised orally

Groups of 10 mice were immunised orally with approx. 5×10^9 cfu of SL3261 alone or carrying pTECH1, or pTECH1-P28, given intragastrically in 0.2ml via a gavage tube. Bleeds taken from week 3 to week 10 showed that most mice receiving the recombinant salmonellae made antibody to TetC as early as week 3 (Figure 8). Mice immunised with the TetC-P28 fusion made antibody to P28 which was detectable in approximately half of the mice by week 8, and then declined (Figure 9).

Antibody responses in mice immunised with the purified fusion protein

Mice were immunised subcutaneously with affinity purified TetC-P28 fusion protein adsorbed on aluminium hy-

dioxide. Controls received commercial tetanus toxoid alone. Preliminary results indicate that animals given the fusion protein make an antibody response to both TetC and to P28 (data not shown). No anti-P28 antibody was detected in mice given tetanus toxoid.

5 T-cell responses to TetC and P28

Mice were immunised i/v with approximately 10^6 cfu of SL3261, SL3261(pTETnir15) and SL3261(pTECH1-P28). Six months later T-cell responses as IL-2/IL-4 production were measured against salmonella whole cell soluble extract, TetC, recombinant P28 and whole adult worm antigen as described in the section headed Materials and Methods below. Table 2 shows that cells from both groups produced an IL-2/IL-4 response to the sodium hydroxide treated salmonella extract and to TetC. However, cells from mice immunised with the salmonellae expressing the TetC-P28 fusion also responded to both recombinant P28 and whole worm extract.

Thus the salmonella delivery system has elicited both humoral and cellular (T-cell) immune responses to P28.

The salmonellae expressing the recombinant antigens all persisted in the mouse tissues as well as the parental strain, and the plasmids were not lost in vivo.

Constructs expressing higher molecular weight fusions (full length P28 and octamer) proved to be the most immunogenic. It may be that the immune response has been promoted by the carrier TetC providing additional T-cell helper epitopes [Francis *et al.* Nature 330: 168-170, 1987]. By week 4 all the mice immunised with cells carrying pTECH1-P28 responded to both TetC and also the full length P28 protein following i/v immunisation. Mice immunised orally also responded to TetC and P28, although not all the mice responded to P28. It may well be that the response to P28, could be improved by boosting. Improved constructs consisting of codon optimised hinge regions, codon optimised P28, and multiple copies of full length P28, are currently in preparation.

The antibody responses to the epitopes improved dramatically with increasing copy number, with the tetramer and octamer "repitope" fusions displaying the greatest potency.

25 EXAMPLE 6

Cloning of HPVE7 protein in pTECH2

The full-length HPV type 16 E7 protein gene was cloned into plasmid pTECH2 by an in frame insertion of the gene in the BamHI site of the vector hinge region.

The E7 gene was obtained from plasmid pGEX16E7 (S.A. Comerford *et al.* J Virology, 65, 4681-90 1991). The gene in this plasmid is flanked by two restriction sites: a 3' BamHI site and a 5' EcoRI site. pGEX16E7 DNA was digested with EcoRI and blunt ended by a filling up reaction using Sequenase (DNA polymerase from USB). It was then digested with BamHI to release the 0.3 Kbp full length E7 gene.

The gel purified gene was ligated to BamHI-EcoRV double digested pTECH2 and this ligation mixture used to transform competent *E.coli* HB101 bacteria.

Recombinant colonies were selected by colony blotting using two monoclonal antibodies against HPV16 E7 protein as probes, namely 6D and 4F (R.W. Tindle, *et al* J Gen. Vir. 71, 1347-54 1990). One of these colonies, named pTE79, was chosen for further analysis.

Protein extracts from pTE79 transformed *E.coli* grown in both aerobic and anaerobic conditions were prepared and analysed by SDS-PAGE and Western blotting. Growth in anaerobic conditions resulted in expression of a recombinant molecule of about 60 KDa which reacted with monoclonal antibodies 6D and 4F and a rabbit polyclonal serum against Tetanus fragment C.

45 EXAMPLE 7

Construction of pTECH2-gD

An immunologically important antigen from herpes simplex virus type 1 [HSV1] is glycoprotein D, termed gD1 (R. J. Watson *et al* Science 218, 381-383 1982). A truncated gD1 gene cassette, lacking the transmembrane and cytoplasmic domains aa26-340, was synthesised by PCR. The PCR primers used are shown in Table 3. The forward primer was designed to encode the N-terminus of the mature protein and the reverse primer encoded the amino acids immediately 5' to the transmembrane domain. In addition the primers were tailored with BamHI and SpeI restriction sites respectively. The template for the PCR reaction was the plasmid pRWFG [a HSV1 gD BamHI-J clone from strain Patton in pBR322; a kind gift from Dr. T. Minson, Cambridge University]. The amplification product was digested with BamHI and SpeI and cloned into pTECH2 which had previously been digested with the respective enzymes.

Expression of the TetC-gD1 fusion protein was assessed by SDS-PAGE and Western blotting of bacterial strains

harbouring the constructs. The Western blots were probed with either anti-TetC polyclonal sera or a monoclonal antibody directed against amino acids 11-19 of the mature gD [designated LP16, obtained from Dr. T. Minson, Cambridge]. The fusion protein is expressed as a 85kDal band visible on Western blots together with lower molecular weight bands down to 50kDal in size. The lower molecular weight bands could correspond to proteolytic cleavage products of gD or represent the products of premature translational termination within the coding region of gD due to ribosomal pausing. The fusion protein is expressed in the salmonella strains SL5338 and SL3261.

EXAMPLE 8

Construction of pTECH2- FMDV/SIV Repeats

Peptides from the foot and mouth disease virus (FMDV, serotype A12) viral protein1 [VP1; aa136-159] and the V2 loop from simian immunodeficiency virus [SIV] envelope protein [gp120; aa171-190] were cloned into pTECH2 (M.P. Broekhuijsen *et al* J. Gen. Virol. 68, 3137-45 1987; K.A. Kent *et al* AIDS Res. and Human Retro. 8:1147-1151 1992).

Complementary oligonucleotides encoding the peptides were designed with a codon selection for optimal expression in *E. coli* [H. Grosjean *et al* Gene, 18, 199-209, 1982]. The oligonucleotides are shown in Table 3. The oligonucleotides were tailored with *Bgl*III and *Spe*I cohesive ends which were generated upon annealing and cloned into pTECH2 which had previously been digested with *Bam*HI and *Spe*I (Figure 3). Dimeric, tetrameric and octameric fusions of these peptides were constructed as described previously.

Expression of the TetC-fusions was assessed by SDS-PAGE and Western blotting with a polyclonal sera directed against TetC and monoclonal antibodies directed against either the FMDV or the SIV epitopes. The FMDV and SIV repeat constructs expressed the TetC fusion proteins in both SL5338 and SL3261.

EXAMPLE 9

Construction of pTECH2- gp120-P28 Peptide Heteromers

To explore the possibility of delivering more than one type of epitope from a single molecule of TetC, fusions have been made with the P28 and SIV repeats to produce a tripartite protein. This form of construction has been facilitated by the modular nature of the vector which allows the assembly of vector modules containing different repeats. These "heteromers" express either tandem dimers or tetramers of the P28 and SIV repeats. To investigate the effect of the position of a particular repeat in the TetC-Repeat A-Repeat B fusion on its expression level, stability, and immunogenicity, the converse combinations have also been constructed i.e. TetC-Repeat B-Repeat A, as is shown in Figure 11. "Heteromers" constructed in this way are TetC-P28 dimer-SIV dimer, TetC-SIV dimer-P28 dimer, TetC-P28 tetramer-SIV tetramer and TetC-SIV tetramer-P28 tetramer.

Expression of the tripartite fusions were evaluated by SDS-PAGE and Western blotting using the antibody reagents described above. These heteromer constructs are all expressed in the *Salmonella* strains SL5338 and SL3261, but intriguingly the expression level and stability is greater in one dimer-dimer and tetramer-tetramer combination (TetC-gp120-P28) than the converse.

EXAMPLE 10

MATERIALS AND METHODS

Plasmids, Oligonucleotides, and the Polymerase Chain Reaction

The plasmid pTETnir15 directs the expression of fragment C from tetanus toxin under the control of the *nirB* promoter [Chatfield *et al. idem* Ozer *et al. idem*]. The TetC-hinge fusion vector pTECH1 was constructed from pTETnir15 by the polymerase chain reaction (PCR) described by Mullis *et al*, 1986. PCR was performed using the high-fidelity thermostable DNA polymerase from *Pyrococcus furiosus*, which possesses an associated 3'-5' exonuclease proofreading activity [K.S. Lundberg *et al* Gene 108: 1-6, 1991]. The amplification reaction was performed according to the manufacturer's instructions (Stratagene).

Bacterial Strains

The bacterial strains used were *E. coli* TG2 (recA; [J. Sambrook *et al*. Molecular cloning: a laboratory manual. Cold Spring Harbor, New York, 1989]), *S. typhimurium* SL5338 (*galE* *r^m*+) [A. Brown J. Infect. Dis. 155: 86-92, *et al* J. Infect. Dis. 155: 86-92, 1987]) and SL3261 (*aroA*); [S.K. Hoiseth *et al* Nature 291, 238-9, 1981]. Bacteria were cultured in

either L or YT broth and on L-agar with ampicillin (50 µg/ml) if appropriate. Plasmid DNA prepared in *E.coli* was first modified by transformation into SL5338 to increase the efficiency of electroporation into the SL3261 *aroA* (*r⁺m) vaccine. For electroporation, cells growing in mid-log phase were harvested and washed in half the initial culture volume of ice-cold water, 1/10 volume of ice-cold glycerol (10%), and finally the cells were resuspended to a concentration of 10¹⁰ cells/ml in ice-cold glycerol (10%). To a pre-chilled cuvette was added a mix of 60 µl cells and 100 ng of plasmid DNA. The cells were pulsed using the Porator from Invitrogen (settings: voltage=1750 µV, capacitance = 40 µF, resistance = 500). Prewarmed L-broth supplemented with 20 mM glucose was added immediately and the cells grown at 37°C with gentle shaking for 1-1.5 h. The cells were then plated on L-agar plates containing ampicillin and incubated at 37°C for 16 h.*

SDS-PAGE and Western Blotting

Expression of the TetC fusions was tested by SDS-PAGE and Western blotting. Cells growing in mid-log phase with antibiotic selection were harvested by centrifugation and the proteins fractionated by 10% SDS-PAGE. The proteins were transferred to a nitrocellulose membrane by electroblotting and reacted with either a polyclonal rabbit antiserum directed against TetC or the full length P28 protein. The blots were then probed with goat anti-rabbit-Ig conjugated to horseradish peroxidase (Dako, UK) and developed with 4-chloro-1-naphthol.

Glutathione-Agarose Affinity Purification

Bacterial cells expressing the TetC full length P28 gene fusion were grown to log phase, chilled on ice, and harvested by centrifugation at 2500Xg for 15 min at 4°C. The cells were resuspended in 1/15th the original volume of ice-cold phosphate buffered saline (PBS) and lysed by sonication in a MSE Soniprep. The insoluble material was removed by centrifugation and to the supernatant was added 1/6 volume of a 50% slurry of pre-swollen glutathione-agarose beads. (Sigma, UK.). After mixing gently at room temperature for 1 h the beads were collected by centrifugation at 1000Xg for 10 sec. The supernatant was discarded and the beads resuspended in 20 volumes of cold PBS-0.5% Triton X-100 and the beads collected again by centrifugation. The washing step was repeated three more times. The fusion protein was eluted by adding 1 volume of 50 mM Tris-HCl, pH 8.0 containing 5.0 mM reduced glutathione (Sigma). After mixing gently for 10 min the beads were pelleted as before and the supernatant removed. The elution step was repeated five more times and the supernatant fractions analysed by SDS-PAGE.

Animals

Female BALB/c mice were purchased from Harlan Olac UK Blackthorn, Bicester, UK, and used when at least 8 weeks of age.

Inoculations and viable counting or organ homogenates

Bacteria were grown in tryptic soy broth (Oxoid) supplemented with 100 µg/ml ampicillin as required. For intravenous inoculation, stationary cultures were diluted in PBS and animals were given approx. 10⁶ cfu in a lateral tail vein in 0.2 ml. For oral inoculation, bacteria were grown in shaken overnight cultures, concentrated by centrifugation, and animals received approximately 5X10⁹ cfu in 0.2 ml intragastrically via a gavage tube. The inoculum doses were checked by viable counts on tryptic soy agar. For viable counts on organ homogenates, groups of 3 mice were sacrificed at intervals, the livers and spleen and (for orally inoculated mice) a pool of mesenteric lymph nodes were homogenised separately in 10 ml distilled water in a Colworth stomacher [C.E. Hormaeche Immunology 37, 311-318, 1979] and viable counts performed on tryptic soy agar supplemented with 100 µg/ml ampicillin.

Measurement of antibody responses

Antibodies were measured by solid phase immunoassay. 96-well-flat bottomed plates were coated with either 0.1 µg of TetC (a kind gift from Dr N Fairweather, the Wellcome Foundation, Beckenham UK) or 1 µg of recombinant P28 (a kind gift from Dr R Pierce, Pasteur Institute, Lille, France) in 100 µl of 0.1 M carbonate buffer, pH 9.6. After overnight incubation at 4°C the plates were incubated for 1 h at 37°C. Blocking of non-specific binding sites was carried out by incubation with 200 µl of 2% casein (BDH, Poole, UK) in PBS pH 7.0 for 1 h at 37°C. Plates were washed three times with 0.05% Tween 20 (Sigma) in PBS with a semiautomatic ELISA washer (Titertek, Flow/ICN, Herts UK). 100 µl of sera from inoculated mice diluted 1:20 in 2% casein was added to each well and the plates were incubated for one hour at 37°C. The plates were washed as above and 100 µl of horse radish peroxidase conjugated goat antimouse immunoglobulins (Dako, Bucks UK), diluted according to the manufacturer's instructions in 2% casein in PBS, was

added to each well and incubated for one hour at 37°C. The plates were washed as above and three more washes were given with PBS alone. The plates were developed using 3,3',3,3'-tetramethylbenzidine dihydrochloride (Sigma) according to the manufacturer's instructions using phosphate/citrate buffer, pH 5.0 and 0.02% hydrogen peroxide. The plates were incubated for 10-15 min at 37°C after which the reaction was stopped with 25 µl 3M H₂SO₄ (BDH). The plates were read in an ELISA reader at 450 nm.

Measurement of T-cell responses

Spleens from mice vaccinated 6 months in advance were removed aseptically and single cell suspensions were prepared by mashing the spleens through a stainless steel sieve with the help of a plastic plunger. Cells were washed once in RPMI1640 medium (Flow/ICN) at 300xg and incubated in Gey's solution to lyse the red cells. White cells were washed twice more as above and resuspended in complete medium, i.e. RPMI1640 supplemented with 100 U/ml penicillin G (Flow/ICN), 100 µg/ml streptomycin (Flow/ICN), 2X10⁻⁵ M B-mercapto-ethanol (Sigma), 1mM N-(2-hydroxyethyl)-piperazine-N'-(2-ethanesulphonic acid) (HEPES) (Flow/ICN) and 10% heat inactivated newborn bovine serum (Northumbria Biolabs, Northumberland, UK). For isolation of T-cells, spleen cells were treated as above and after lysis of red cells the white cells were resuspended in warm (37°C) RPMI1640 and passed through a Wigzell glass bead column [H. Wigzell, *et al* Scand. J. Immunol 1: 75-87, 1972].

Cells were plated at 2X10⁶/ml in a final volume of 200 µl of complete medium in 96-well plates in the presence of the relevant antigens. These were either an alkali-treated whole cell soluble extract of *S.typhimurium* C5 prepared as described in Villarreal *et al.* [Microbial Pathogenesis 13: 305-315, 1992] at 20 µg/ml final concentration; TetC at 10 µg/ml; recombinant *Schistosoma mansoni* P28 at 50 µg/ml; and *S. mansoni* whole adult worm extract (a kind gift from Dr D Dunne, Cambridge University) at 20 µg/ml. Cells were incubated in a 95% humidity, 5% CO₂, 37°C atmosphere.

Feeder cells for T-cells for animals immunised with SL3261(pTECH1-P28) were obtained from syngeneic BALB/c naive spleens prepared as above. For mice immunised with pTETnir15, feeder cells were obtained from similarly immunised animals. After red cell lysis and two washes with RPMI1640 cells were X-ray irradiated at 2000 rads and washed twice more. These antigen presenting cells were resuspended in complete medium to give a final ratio of 1:1 with T-cells.

IL-2 production and assay

T-cell suspensions were plated as above. After two days, 50 µl of supernatant was harvested and added to 1x10⁴ cells/well CTLL-2(IL-2 dependent) in 50 µl of medium. CTLL-2 cells were obtained from Dr J Ellis, University College, London UK and maintained in RPMI1640 supplemented as above, substituting the newborn bovine serum for foetal bovine serum. After 20 h, 20 µl of MTT at a concentration of 5 mg/ml in PBS were added. MTT transformation was measured as indicated elsewhere [Tada *et al.* J. Immunol. Methods 93: 157-165, 1986]. results were expressed as the mean of the optical density of triplicates read at 570 nm using a reference filter of 630 nm. Significance was determined by Student's t-test.

BACTERIAL SAMPLE DEPOSITS

Salmonella typhimurium strains SL3261-pTECH1, SL3261-pTECH1-P28, SL3261-pTECH2, SL3261-pTECH2-P28 Octamer and PTE79 have been deposited at the National Collection of Type Cultures, 61 Colindale Avenue, London, NW9 5HT, UK, on 15th July 1993 under Deposit Numbers NCTC 12831, NCTC 12833, 12832, 12834 and 12837 respectively.

TABLE 1**DNA SEQUENCES OF OLIGONUCLEOTIDES UTILISED IN THE
CONSTRUCTION OF THE TETC-HINGE VECTORS****A). Primer 1. Sense PCR (21mer). (SEQ ID NO: 4)**

SacII

5'AAA GAC TCC GCG GGC GAA GTT -3'

TETANUS TOXIN C FRAGMENT SEQ.

B).Primer 2. Anti-Sense PCR Primer (64mer). (SEQ ID NO: 5)

BamHI

STOP

SpeI

XbaI

HINGE REGION

5'- CTAT GGA TCC TTA ACT AGT GAT TCT AGA GGG CCC GGG CCC

GTC GTT GGT CCA ACC TTC ATC GGT -3'

TETANUS TOXIN C FRAGMENT SEQ. 3'-END

C). The pTECH2 Linker (SEQ ID NO: 6)

XbaI BamHI EcoRV HindIII SpeI Stop XBamHI*

5'-CTAGA GGATCC GATATC AAGCTT ACTAGT TAA T-3'

3'-T CCTAGG CTATAG TTCGAA TGATCA ATT ACTAG-5'

*This BamHI recognition sequence is now destroyed.

TABLE 2

T-Cell responses (IL-2/IL-4 production) elicited by alkali treated salmonella whole cell extract (C5NaOH), TetC, *Schistosoma mansoni* whole adult worm antigen (SWA), and recombinant P28 in mice immunised with SL3261 (pTETnir15) or SL3261(pTECH1.P28).

Immunising strain	Stimulating antigen				
	none	CSNaOH	TetC	P28	SWA
SL3261 (pTETnir15)	2±4	67±5	41±1	0	0

TABLE 2 (continued)

T-Cell responses (IL-2/IL-4 production) elicited by alkali treated salmonella whole cell extract (C5NaOH), TetC, *Schistosoma mansoni* whole adult worm antigen (SWA), and recombinant P28 in mice immunised with SL3261 (pTETnir15) or SL3261(pTECH1.P28).

Immunising strain	none	CSNaOH	Stimulating antigen		
			TetC	P28	SWA
SL3261 (pTECH1-P28)	6±2.6	109+10	50±8	25±8 p<0.001	17±6 p<0.01
Results expressed as (A ₅₇₀ -A ₆₃₀) x 1000±S.D.					

TABLE 3Oligonucleotide Sequences for HSV, FMDV, and SIV.HSV1 gD Gene

PCR Primer 1: 5'-AATGGATCCAAATATGCCCTGGCGGATGC-3'
(SEQ ID NO: 7)

PCR Primer 2: 5'-TTAACTAGTGTGTTTCGGGGTGGCCGGGGGAT-3'
(SEQ ID NO: 8)

FMDV VP1 Epitope

Oligo 1:
5'-GATCTAAATACTCTGCTTCTGGTTCTGGTGTTCGTGGTGAC
TTCGGTTCTCTGGCTCCGCGTGTGCTCGTCAGCTGA-3'
(SEQ ID NO: 9)

Oligo 2:
5'-CTAGTCAGCTGACGAGCAACACGCGGAGCCAGAGAACCGAA
GTCACCACGAACACCAGAACCAGAAGCAGAGTATTTA-3
(SEQ ID NO: 10)

SIV gp120 Epitope

Oligo 1:
5'-GATCTAACATGACCGGTCTGAAACGTGATAAAACCAAAGAA
TACAACGAAACCTGGTACTCTACCA-3'
(SEQ ID NO: 11)

Oligo 2:
5'-CTAGTGGTAGAGTACCAGGTTTCGTTGTATTCTTTGGTTTT
ATCACGTTTCAGACCGGTCATGTTA-3'
(SEQ ID NO: 12)

Sm P28 Gene

PCR Primer 1: 5'-TAGTCTAGAATGGCTGGCGAGCATATCAAG-3'
(SEQ ID NO: 13)

PCR Primer 2: 5'-TTAGGATCCTTAGAAGGGAGTTGCAGGCCT-3'
(SEQ ID NO: 14)

Sm P28 Epitope

Oligo 1:
5'-GATCTAAACCGCAGGAAGAAAAAGAAAAATCACCAAAGAAA
TCCTGAACGGCAAAA-3'
(SEQ ID NO: 15)

Oligo 2:
5'-CTAGTTTTGCCGTTTCAGGATTCTTTGGTGATTTTTCTTTTTCT
TCCTGCGGTTTA-3'
(SEQ ID NO: 16)

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: MEDEVA HOLDINGS BV
(B) STREET: CHURCHILL-LAAN 223
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(F) POSTAL CODE (ZIP): 1078 ED

(ii) TITLE OF INVENTION: VACCINES

(iii) NUMBER OF SEQUENCES: 20

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: GB 9216317.9
(B) FILING DATE: 31-JUL-1992

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: GB 9306398.0
(B) FILING DATE: 26-MAR-1993

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Escherichia coli

(ix) FEATURE:

(A) NAME/KEY: promoter
(B) LOCATION: 1..61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AATTCAGGTA AATTTGATGT ACATCAAATG GTACCCCTTG CTGAATCGTT AAGGTAGGCG

60

5

GTAGGGCC

68

(2) INFORMATION FOR SEQ ID NO: 2:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

20

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

25

AATTCAGGTA AATTTGATGT ACATCAAATG GTACCCCTTG CTGAATCGTT AAGGTAGGCG

60

GTAGGGCC

68

30

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

35

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

40

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTACCGCCTA CCTTAACGAT TCAGCAAGGG GTACCATTG ATGTACATCA AATTTACCTG

60

50

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

AAAGACTCCG CGGGCGAAGT T

21

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CTATGGATCC TTAAGTAGTG ATTCTAGAGG GCCCCGGCCC GTCGTTGGTC CAACCTTCAT

60

CGGT

64

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CTAGAGGATC CGATATCAAG CTTACTAGTT AAT

33

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

10

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

15

AATGGATCCA AATATGCCCT GGCGGATGC

29

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

30

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

35

TAACTAGTGT TGTTCTGGGGT GGCCGGGGGA T

31

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

50

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

55

GATCTAAATA CTCTGCTTCT GGTTCCTGGTG TTCGTGGTGA CTTCGGTTCT CTGGCTCCGC

60

GTGTTGCTCG TCAGCTGA

78

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CTAGTCAGCT GACGAGCAAC ACGCGGAGCC AGAGAACCGA AGTCACCACG AACACCAGAA 60
 CCAGAAGCAG AGTATTTA 78

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GATCTAACAT GACCGGTCTG AAACGTGATA AAACCAAAGA ATACAACGAA ACCTGGTACT 60
 CTACCA 66

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CTAGTGGTAG AGTACCAGGT TTCGTTGTAT TCTTTGGTTT TATCACGTTT CAGACCGGTC 60
 5 ATGTTA 66

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

25 TAGTCTAGAA TGGCTGGCGA GCATATCAAG 30

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

45 TTAGGATCCT TAGAAGGGAG TTGCAGGCCT 30

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GATCTAAACC GCAGGAAGAA AAAGAAAAAA TCACCAAAGA AATCCTGAAC GGCAAAA

57

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CTAGTTTTGC CGTTCAGGAT TTCTTTGGTG ATTTTTTCTT TTTCTTCCTG CGGTTTA

57

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3754 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TTCAGGTAAA TTTGATGTAC ATCAAATGGT ACCCCTTGCT GAATCGTTAA GGTAGGCGGT

60

AGGGCCCAGA TCTTAATCAT CCACAGGAGA CTTTCTGATG AAAAACCTTG ATTGTTGGGT

120

	CGACAACGAA GAAGACATCG ATGTTATCCT GAAAAAGTCT ACCATTCTGA ACTTGGACAT	180
5	CAACAACGAT ATTATCTCCG ACATCTCTGG TTTCAACTCC TCTGTTATCA CATATCCAGA	240
	TGCTCAATTG GTGCCGGGCA TCAACGGCAA AGCTATCCAC CTGGTTAACA ACGAATCTTC	300
	TGAAGTTATC GTGCACAAGG CCATGGACAT CGAATACAAC GACATGTTCA ACAACTTCAC	360
10	CGTTAGCTTC TGGCTGCGCG TTCCGAAAGT TTCTGCTTCC CACCTGGAAC AGTACGGCAC	420
	TAACGAGTAC TCCATCATCA GCTCTATGAA GAAACACTCC CTGTCCATCG GCTCTGGTTG	480
15	GTCTGTTTCC CTGAAGGGTA ACAACCTGAT CTGGACTCTG AAAGACTCCG CGGGCGAAGT	540
	TCGTCAGATC ACTTTCGCGG ACCTGCCGGA CAAGTTCAAC GCGTACCTGG CTAACAAATG	600
	GGTTTTTCATC ACTATCACTA ACGATCGTCT GTCTTCTGCT AACCTGTACA TCAACGGCGT	660
20	TCTGATGGGC TCCGCTGAAA TCACTGGTCT GGGCGCTATC CGTGAGGACA ACAACATCAC	720
	TCTTAAGCTG GACCGTTGCA ACAACAACAA CCAGTACGTA TCCATCGACA AGTTCCGTAT	780
25	CTTCTGCAAA GCACTGAACC CGAAAGAGAT CGAAAACTG TATACCAGCT ACCTGTCTAT	840
	CACCTTCCTG CGTGACTTCT GGGGTAACCC GCTGCGTTAC GACACCGAAT ATTACCTGAT	900
	CCCGGTAGCT TCTAGCTCTA AAGACGTTCA GCTGAAAAAC ATCACTGACT ACATGTACCT	960
30	GACCAACGCG CCGTCCTACA CTAACGGTAA ACTGAACATC TACTACCGAC GTCTGTACAA	1020
	CGGCCTGAAA TTCATCATCA AACGCTACAC TCCGAACAAC GAAATCGATT CTTTCGTTAA	1080
35	ATCTGGTGAC TTCATCAAAC TGTACGTTTC TTACAACAAC AACGAACACA TCGTTGGTTA	1140
	CCCGAAAGAC GGTAACGCTT TCAACAACCT GGACAGAATT CTGCGTGTTG GTTACAACGC	1200
	TCCGGGTATC CCGCTGTACA AAAAAATGGA AGCTGTAAAA CTGCGTGACC TGAAAACTA	1260
40	CTCTGTTTCTAG CTGAACTGT ACGACGACAA AAACGCTTCT CTGGGTCTGG TTGGTACCCA	1320
	CAACGGTCAG ATCGGTAACG ACCCGAACCG TGACATCCTG ATCGCTTCTA ACTGGTACTT	1380
45	CAACCACCTG AAAGACAAAA TCCTGGGTTG CGACTGGTAC TTCGTTCCGA CCGATGAAGG	1440
	TTGGACCAAC GACGGGCCGG GGGCTCTAG AATCACTAGT TAAGGATCCG CTAGCCCGCC	1500
	TAATGAGCGG GCTTTTTTTT CTCGGGCAGC GTTGGGTCCT GGCCACGGGT GCGCATGATC	1560
50	GTGCTCCTGT CGTTGAGGAC CCGGCTAGGC TGGCGGGGTT GCCTTACTGG TTAGCAGAAT	1620
	GAATCACCGA TACGCGAGCG AACGTGAAGC GACTGCTGCT GCAAAACGTC TGCGACCTGA	1680
55	GCAACAACAT GAATGGTCTT CGGTTTCCGT GTTTCGTAAA GTCTGGAAAC GCGGAAGTCA	1740
	GCGCTCTTCC GCTTCCTCGC TCACTGACTC GCTGCGCTCG GTCGTTCCGC TGCGGCGAGC	1800

	GGTATCAGCT CACTCAAAGG CGGTAATACG GTTATCCACA GAATCAGGGG ATAACGCAGG	1860
	AAAGAACATG TGAGCAAAAG GCCAGCAAAA GGCCAGGAAC CGTAAAAAGG CCGCGTTGCT	1920
5	GGCGTTTTTC CATAGGCTCC GCCCCCTGA CGAGCATCAC AAAAATCGAC GCTCAAGTCA	1980
	GAGGTGGCGA AACCCGACAG GACTATAAAG ATACCAGGCG TTTCCCCCTG GAAGCTCCCT	2040
10	CGTGCGCTCT CCTGTTCCGA CCCTGCCGCT TACCGGATAC CTGTCCGCCT TTCTCCCTTC	2100
	GGGAAGCGTG GCGCTTTCTC AATGCTCACG CTGTAGGTAT CTCAGTTCGG TGTAGGTCGT	2160
	TCGCTCCAAG CTGGGCTGTG TGCACGAACC CCCCCTTCAG CCCGACCGCT GCGCCTTATC	2220
15	CGGTAACAT CTGCTTGAGT CCAACCCGGT AAGACACGAC TTATCGCCAC TGGCAGCAGC	2280
	CACTGGTAAC AGGATTAGCA GAGCGAGGTA TGTAGGCGGT GCTACAGAGT TCTTGAAGTG	2340
20	GTGGCCTAAC TACGGCTACA CTAGAAGGAC AGTATTTGGT ATCTGCGCTC TGCTGAAGCC	2400
	AGTTACCTTC GGAAAAAGAG TTGGTAGCTC TTGATCCGGC AAACAAACCA CCGCTGGTAG	2460
	CGGTGGTTTT TTTGTTTGCA AGCAGCAGAT TACGCGCAGA AAAAAAGGAT CTCAAGAAGA	2520
25	TCCTTTGATC TTTTCTACGG GGTCTGACGC TCAGTGAAC GAAAACTCAC GTTAAGGGAT	2580
	TTTGGTCATG AGATTATCAA AAAGGATCTT CACCTAGATC CTTTTAAATT AAAAATGAAG	2640
30	TTTTAAATCA ATCTAAAGTA TATATGAGTA AACTTGGTCT GACAGTTACC AATGCTTAAT	2700
	CAGTGAGGCA CCTATCTCAG CGATCTGTCT ATTTCTGTTCA TCCATAGTTG CCTGACTCCC	2760
	CGTCGTGTAG ATAACACGA TACGGGAGGG CTTACCATCT GGCCCCAGTG CTGCAATGAT	2820
35	ACCGCGAGAC CCACGCTCAC CGGCTCCAGA TTTATCAGCA ATAAACCAGC CAGCCGGAAG	2880
	GGCCGAGCGC AGAAGTGGTC CTGCAACTTT ATCCGCCTCC ATCCAGTCTA TTAATTGTTG	2940
40	CCGGGAAGCT AGAGTAAGTA GTTCGCCAGT TAATAGTTTG CGCAACGTTG TTGCCATTGC	3000
	TGCAGGCATC GTGGTGTAC GCTCGTCGTT TGGTATGGCT TCATTTCAGCT CCGGTTCCCA	3060
	ACGATCAAGG CGAGTTACAT GATCCCCCAT GTTGTGCAAA AAAGCGGTTA GCTCCTTCGG	3120
45	TCCTCCGATC GTTGTGAGAA GTAAGTTGGC CGCAGTGTTA TCACTCATGG TTATGGCAGC	3180
	ACTGCATAAT TCTCTTACTG TCATGCCATC CGTAAGATGC TTTTCTGTGA CTGGTGAGTA	3240
50	CTCAACCAAG TCATTCTGAG AATAGTGTAT GCGGCGACCG AGTTGCTCTT GCCCGGCGTC	3300
	AACACGGGAT AATACCGCGC CACATAGCAG AACTTTAAAA GTGCTCATCA TTGGAAAACG	3360
	TTCTTCGGGG CGAAAACTCT CAAGGATCTT ACCGCTGTTG AGATCCAGTT CGATGTAACC	3420
55	CACTCGTGCA CCCAACTGAT CTTTCAGCATC TTTTACTTTC ACCAGCGTTT CTGGGTGAGC	3480

AAAAACAGGA AGGCAAAATG CCGCAAAAAA GGAATAAGG GCGACACGGA AATGTTGAAT 3540
 ACTCATACTC TTCCTTTTTC AATATTATTG AAGCATTAT CAGGGTTATT GTCTCATGAG 3600
 5 CGGATACATA TTTGAATGTA TTTAGAAAAA TAAACAAATA GGGGTTCCGC GCACATTTC 3660
 CCGAAAAGTG CCACCTGACG TCTAAGAAAC CATTATTATC ATGACATTAA CCTATAAAAA 3720
 10 TAGGCGTATC ACGAGGCCCT TTCGTCTTCA AGAA 3754

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3769 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

30 TTCAGGTAAA TTTGATGTAC ATCAAATGGT ACCCCTTGCT GAATCGTTAA GGTAGGCGGT 60
 AGGGCCCAGA TCTTAATCAT CCACAGGAGA CTTTCTGATG AAAACCTTG ATTGTTGGGT 120
 35 CGACAACGAA GAAGACATCG ATGTTATCCT GAAAAAGTCT ACCATTCTGA ACTTGGACAT 180
 CAACAACGAT ATTATCTCCG ACATCTCTGG TTCAACTCC TCTGTTATCA CATATCCAGA 240
 TGCTCAATTG GTGCCGGGCA TCAACGGCAA AGCTATCCAC CTGGTTAACA ACGAATCTTC 300
 40 TGAAGTTATC GTGCACAAGG CCATGGACAT CGAATACAAC GACATGTTCA ACAACTTCAC 360
 CGTTAGCTTC TGGCTGCGCG TTCCGAAAGT TTCTGCTTCC CACCTGGAAC AGTACGGCAC 420
 TAACGAGTAC TCCATCATCA GCTCTATGAA GAAACACTCC CTGTCCATCG GCTCTGGTTG 480
 45 GTCTGTTTCC CTGAAGGGTA ACAACCTGAT CTGGACTCTG AAAGACTCCG CGGGCGAAGT 540
 TCGTCAGATC ACTTTCCGCG ACCTGCCGGA CAAGTTCAAC GCGTACCTGG CTAACAAATG 600
 50 GGTTTTCATC ACTATCACTA ACGATCGTCT GTCTTCTGCT AACCTGTACA TCAACGGCGT 660
 TCTGATGGGC TCCGCTGAAA TCACTGGTCT GGGCGCTATC CGTGAGGACA ACAACATCAC 720
 55 TCTTAAGCTG GACCGTTGCA ACAACAACAA CCAGTACGTA TCCATCGACA AGTTCCGTAT 780
 CTTCTGCAAA GCACTGAACC CGAAAGAGAT CGAAAACTG TATACCAGCT ACCTGTCTAT 840

	CACCTTCCTG CGTGACTTCT GGGGTAACCC GCTGCGTTAC GACACCGAAT ATTACCTGAT	900
	CCCGGTAGCT TCTAGCTCTA AAGACGTTCA GCTGAAAAAC ATCACTGACT ACATGTACCT	960
5	GACCAACGCG CCGTCCTACA CTAACGGTAA ACTGAACATC TACTACCGAC GTCTGTACAA	1020
	CGGCCTGAAA TTCATCATCA AACGCTACAC TCCGAACAAC GAAATCGATT CTTTCGTTAA	1080
10	ATCTGGTGAC TTCATCAAAC TGTACGTTTC TTACAACAAC AACGAACACA TCGTTGGTTA	1140
	CCCGAAAGAC GGTAACGCTT TCAACAACCT GGACAGAATT CTGCGTGTTG GTTACAACGC	1200
	TCCGGGTATC CCGCTGTACA AAAAAATGGA AGCTGTATAA CTGCGTGACC TGAAAAACCTA	1260
15	CTCTGTTTCTAG CTGAAACTGT ACGACGACAA AAACGCTTCT CTGGGTCTGG TTGGTACCCA	1320
	CAACGGTCAG ATCGGTAACG ACCCGAACCG TGACATCCTG ATCGCTTCTA ACTGGTACTT	1380
20	CAACCACCTG AAAGACAAAA TCCTGGGTTG CGACTGGTAC TTCGTTCCGA CCGATGAAGG	1440
	TTGGACCAAC GACGGGCCGG GGCCCTCTAG AGGATCCGAT ATCAAGCTTA CTAGTTAATG	1500
	ATCCGCTAGC CCGCCTAATG AGCGGGCTTT TTTTCTCGG GCAGCGTTGG GTCCTGGCCA	1560
25	CGGGTGCGCA TGATCGTGCT CCTGTGCTTG AGGACCCGGC TAGGCTGGCG GGGTTGCCTT	1620
	ACTGGTTAGC AGAATGAATC ACCGATACGC GAGCGAACGT GAAGCGACTG CTGCTGCAAA	1680
30	ACGTCTGCGA CCTGAGCAAC AACATGAATG GTCTTCGGTT TCCGTGTTTC GTAAAGTCTG	1740
	GAAACGCGGA AGTCAGCGCT CTTCCGCTTC CTCGCTCACT GACTCGCTGC GCTCGGTCGT	1800
	TCGGCTGCGG CGAGCGGTAT CAGCTCACTC AAAGGCGGTA ATACGGTTAT CCACAGAATC	1860
35	AGGGGATAAC GCAGGAAAGA ACATGTGAGC AAAAGGCCAG CAAAAGGCCA GGAACCGTAA	1920
	AAAGGCCGCG TTGCTGGCGT TTTTCCATAG GCTCCGCCCC CCTGACGAGC ATCACAACAAA	1980
40	TCGACGCTCA AGTCAGAGGT GGCGAAACCC GACAGGACTA TAAAGATACC AGGCGTTTCC	2040
	CCCTGGAAGC TCCCTCGTGC GCTCTCCTGT TCCGACCCTG CCGCTTACCG GATACCTGTC	2100
	CGCCTTTCTC CTTTCGGGAA GCGTGGCGCT TTCTCAATGC TCACGCTGTA GGTATCTCAG	2160
45	TTGCGGTGTAG GTCGTTGCT CCAAGCTGGG CTGTGTGCAC GAACCCCCCG TTCAGCCCGA	2220
	CCGCTGCGCC TTATCCGTA ACTATCGTCT TGAGTCCAAC CCGGTAAGAC ACGACTTATC	2280
50	GCCACTGGCA GCAGCCACTG GTAACAGGAT TAGCAGAGCG AGGTATGTAG GCGGTGCTAC	2340
	AGAGTTCTTG AAGTGGTGGC CTAACACGG CTACACTAGA AGGACAGTAT TTGGTATCTG	2400
	CGCTCTGCTG AAGCCAGTTA CCTTCGAAA AAGAGTTGGT AGCTCTTGAT CCGGCAACAA	2460
55	AACCACCGCT GGTAGCGGTG GTTTTTTTGT TTGCAAGCAG CAGATTACGC GCAGAAAAAA	2520

AGGATCTCAA GAAGATCCTT TGATCTTTTC TACGGGGTCT GACGCTCAGT GGAACGAAAA 2580
 CTCACGTTAA GGGATTTTGG TCATGAGATT ATCAAAAAGG ATCTTCACCT AGATCCTTTT 2640
 5 AAATTAAAAA TGAAGTTTTA AATCAATCTA AAGTATATAT GAGTAAACTT GGTCTGACAG 2700
 TTACCAATGC TTAATCAGTG AGGCACCTAT CTCAGCGATC TGTCTATTTT GTTCATCCAT 2760
 10 AGTTGCCTGA CTCCCCGTCG TGTAGATAAC TACGATACGG GAGGGCTTAC CATCTGGCCC 2820
 CAGTGCTGCA ATGATACCGC GAGACCCACG CTCACCGGCT CCAGATTTAT CAGCAATAAA 2880
 15 CCAGCCAGCC GGAAGGGCCG AGCGCAGAAG TGGTCCTGCA ACTTTATCCG CCTCCATCCA 2940
 GTCTATTAAT TGTTGCCGGG AAGCTAGAGT AAGTAGTTCT CCAGTTAATA GTTGCGCAA 3000
 CGTTGTTGCC ATTGCTGCAG GCATCGTGGT GTCACGCTCG TCGTTTGGTA TGGCTTCATT 3060
 20 CAGCTCCGGT TCCCAACGAT CAAGGCGAGT TACATGATCC CCCATGTTGT GCAAAAAAGC 3120
 GGTTAGCTCC TTCGGTCCTC CGATCGTTGT CAGAAGTAAG TTGGCCGCAG TGTTATCACT 3180
 25 CATGGTTATG GCAGCACTGC ATAATTCTCT TACTGTCATG CCATCCGTAA GATGCTTTTC 3240
 TGTGACTGGT GAGTACTCAA CCAAGTCATT CTGAGAATAG TGTATGCGGC GACCGAGTTG 3300
 CTCTTGCCCG GCGTCAACAC GGGATAATAC CGCGCCACAT AGCAGAACTT TAAAGTGCT 3360
 30 CATCATTGGA AAACGTTCTT CGGGGCGAAA ACTCTCAAGG ATCTTACCGC TGTGAGATC 3420
 CAGTTCGATG TAACCCACTC GTGCACCCAA CTGATCTTCA GCATCTTTTA CTTTCACCAG 3480
 35 CGTTTCTGGG TGAGCAAAAA CAGGAAGGCA AAATGCCGCA AAAAAGGGAA TAAGGGCGAC 3540
 ACGGAAATGT TGAATACTCA TACTCTTCCT TTTTCAATAT TATTGAAGCA TTTATCAGGG 3600
 TTATTGTCTC ATGAGCGGAT ACATATTTGA ATGTATTTAG AAAAATAAAC AAATAGGGGT 3660
 40 TCCGCGCACA TTTCCCCGAA AAGTGCCACC TGACGTCTAA GAAACCATTA TTATCATGAC 3720
 ATTAACCTAT AAAAATAGGC GTATCACGAG GCCCTTTCGT CTTCAAGAA 3769

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TCTAGAGGAT CCGATATCAA GCTTACTAGT TAATGATC

38

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Gly Pro Gly Pro Ser Arg Gly Ser Asp Ile Lys Leu Thr Ser
1 5 10

Claims

1. A vaccine composition comprising a pharmaceutically acceptable carrier and an attenuated bacterium containing a DNA construct comprising a promoter which is capable of promoting expression of a sequence under, and has activity which is induced under, anaerobic conditions, the promoter being operably linked to a DNA sequence encoding first and second proteins linked by a chain of amino acids defining a hinge region.
2. A vaccine composition according to claim 1 wherein the promoter is the nirB promoter or a part or derivative thereof which is capable of promoting expression of a sequence under anaerobic conditions.
3. A vaccine composition according to claim 1 or claim 2 wherein the hinge region comprises proline and/or glycine amino acids.
4. A vaccine composition according to any one of the preceding claims wherein the first protein is an antigenic sequence comprising tetanus toxin C fragment or epitopes thereof.
5. A vaccine composition according to any one of the preceding claims wherein the second protein is an antigenic determinant of a pathogenic microorganism.
6. A vaccine composition according to claim 5 wherein the antigenic determinant is an antigenic sequence derived from a virus, bacterium, fungus, yeast or parasite.
7. A vaccine composition according to claim 6 wherein the antigenic sequence is derived from the P28 protein of Schistosoma mansoni.
8. A vaccine composition according to claim 6 wherein the antigenic sequence is derived from human papilloma virus (HPV).
9. A vaccine composition according to claim 6 wherein the antigenic sequence is derived from herpes simplex virus.
10. A vaccine composition according to claims 6 wherein the antigenic sequence is derived from Foot-and-Mouth virus (FMDV).

11. A vaccine composition according to any one of the preceding claims wherein the attenuated bacterium is selected from the genus Salmonella.

5 Patentansprüche

1. Impfstoffzusammensetzung, umfassend einen pharmazeutisch annehmbaren Träger und ein attenuiertes Bakterium, enthaltend ein DNA-Konstrukt, das einen Promotor umfaßt, der in der Lage ist, die Expression einer Sequenz unter anaeroben Bedingungen zu fördern und Aktivität aufweist, die unter anaeroben Bedingungen induziert wird, wobei der Promoter funktionstüchtig mit einer DNA-Sequenz verknüpft ist, die für erste und zweite Proteine codiert, welche verknüpft sind durch eine Kette von Aminosäuren, die eine Gelenkregion definiert.
2. Impfstoffzusammensetzung gemäß Anspruch 1, wobei der Promotor der nirB-Promotor oder ein Teil oder ein Derivat davon ist, der in der Lage ist, die Expression einer Sequenz unter anaeroben Bedingungen zu fördern.
3. Impfstoffzusammensetzung gemäß Anspruch 1 oder Anspruch 2, wobei die Gelenkregion Prolin- und/oder Glycin-Aminosäuren umfaßt.
4. Impfstoffzusammensetzung gemäß irgendeinem der vorstehenden Ansprüche, wobei das erste Protein eine antigene Sequenz ist, welche ein Tetanus-Toxin-C-Fragment oder Epitope davon umfaßt.
5. Impfstoffzusammensetzung gemäß irgendeinem der vorstehenden Ansprüche, wobei das zweite Protein eine antigene Determinante eines pathogenen Mikroorganismus ist.
6. Impfstoffzusammensetzung gemäß Anspruch 5, wobei die antigene Determinante eine antigene Sequenz, abgeleitet aus einem Virus, Bakterium, Pilz, Hefe oder Parasiten, ist.
7. Impfstoffzusammensetzung gemäß Anspruch 6, wobei die antigene Sequenz von dem P28-Protein von Schistosoma mansoni abgeleitet ist.
8. Impfstoffzusammensetzung gemäß Anspruch 6, wobei die antigene Sequenz aus humanem Papillomvirus (HPV) abgeleitet ist.
9. Impfstoffzusammensetzung gemäß Anspruch 6, wobei die antigene Sequenz aus Herpes Simplex-Virus abgeleitet ist.
10. Impfstoffzusammensetzung gemäß Anspruch 6, wobei die antigene Sequenz aus Maul-und-Klauenseuchen-Virus (FMDV) abgeleitet ist.
11. Impfstoffzusammensetzung gemäß irgendeinem der vorstehenden Ansprüche, wobei das attenuierte Bakterium aus der Gattung Salmonella gewählt ist.

45 Revendications

1. Une composition de vaccin comprenant un véhicule pharmaceutiquement acceptable et une bactérie atténuée contenant une construction d'ADN comprenant un promoteur qui est capable de promouvoir l'expression d'une séquence, et a une activité qui est induite dans des conditions anaérobies, le promoteur étant lié de manière fonctionnelle à une séquence d'ADN codant pour une première et une seconde protéine liées par une chaîne d'acides aminés définissant une région charnière.
2. Une composition de vaccin selon la revendication 1 dans laquelle le promoteur est le promoteur nirB ou une partie ou un dérivé de celui-ci qui est capable de promouvoir l'expression d'une séquence dans des conditions anaérobies.
3. Une composition de vaccin selon la revendication 1 ou la revendication 2 dans laquelle la région charnière comprend des acides aminés proline et/ou glycine.

4. Une composition de vaccin selon l'une quelconque des revendications précédentes dans laquelle la première protéine est une séquence antigénique comprenant le fragment C de la toxine du tétanos ou des épitopes de celui-ci.
5. Une composition de vaccin selon l'une quelconque des revendications précédentes dans laquelle la seconde protéine est un déterminant antigénique d'un micro-organisme pathogène.
6. Une composition de vaccin selon la revendication 5 dans laquelle le déterminant antigénique est une séquence antigénique provenant d'un virus, d'une bactérie, d'un champignon, d'une levure ou d'un parasite.
7. Une composition de vaccin selon la revendication 6 dans laquelle la séquence antigénique provient de la protéine P28 de Schistosoma mansoni.
8. Une composition de vaccin selon la revendication 6 dans laquelle la séquence antigénique provient du papillomavirus humain (HPV).
9. Une composition de vaccin selon la revendication 6 dans laquelle la séquence antigénique provient du virus Herpes simplex.
10. Une composition de vaccin selon la revendication 6 dans laquelle la séquence antigénique provient de l'aphtovirus (FMDV).
11. Une composition de vaccin selon l'une quelconque des revendications précédentes dans laquelle la bactérie atténuée est choisie dans le genre Salmonella.

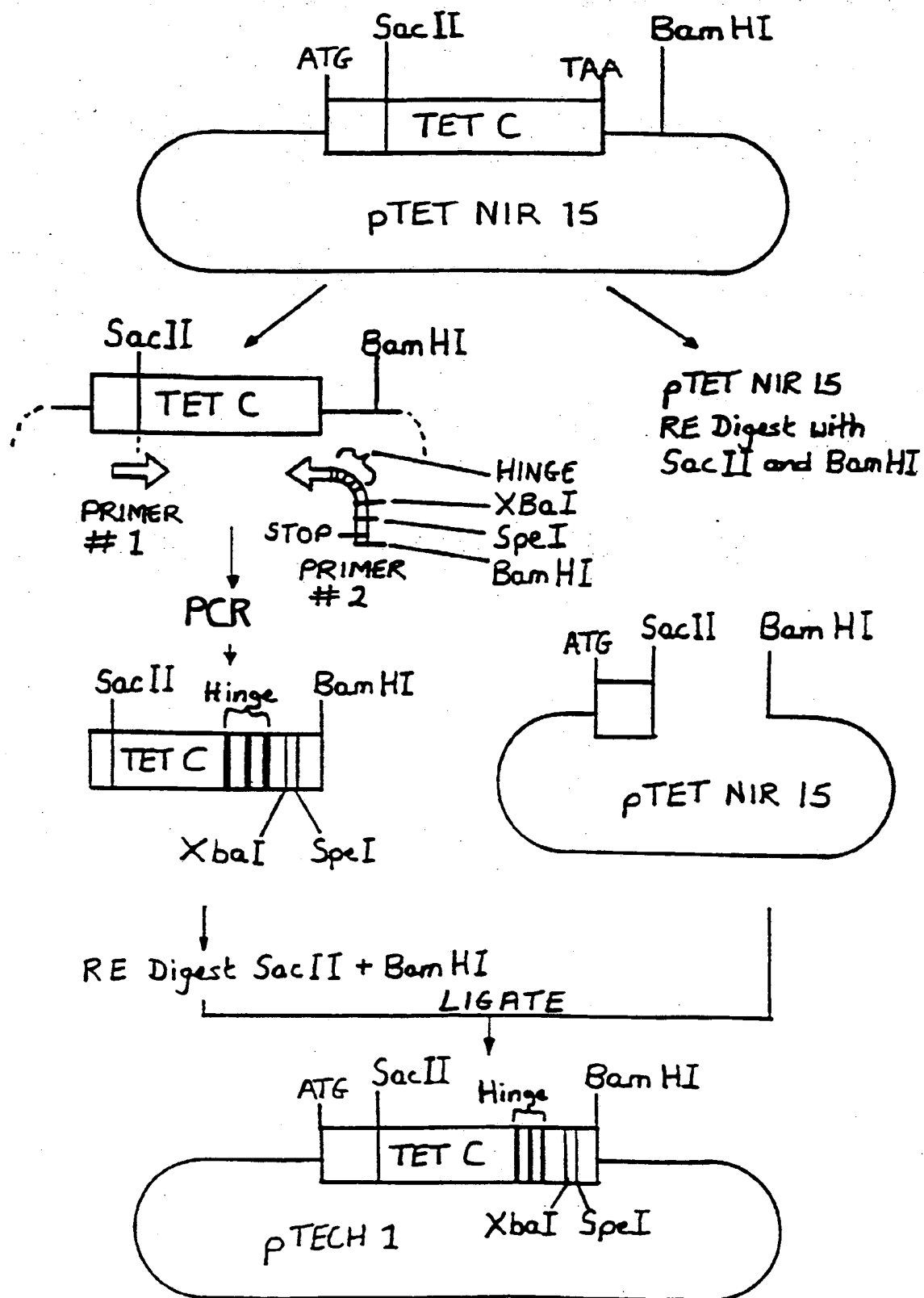


FIGURE 1

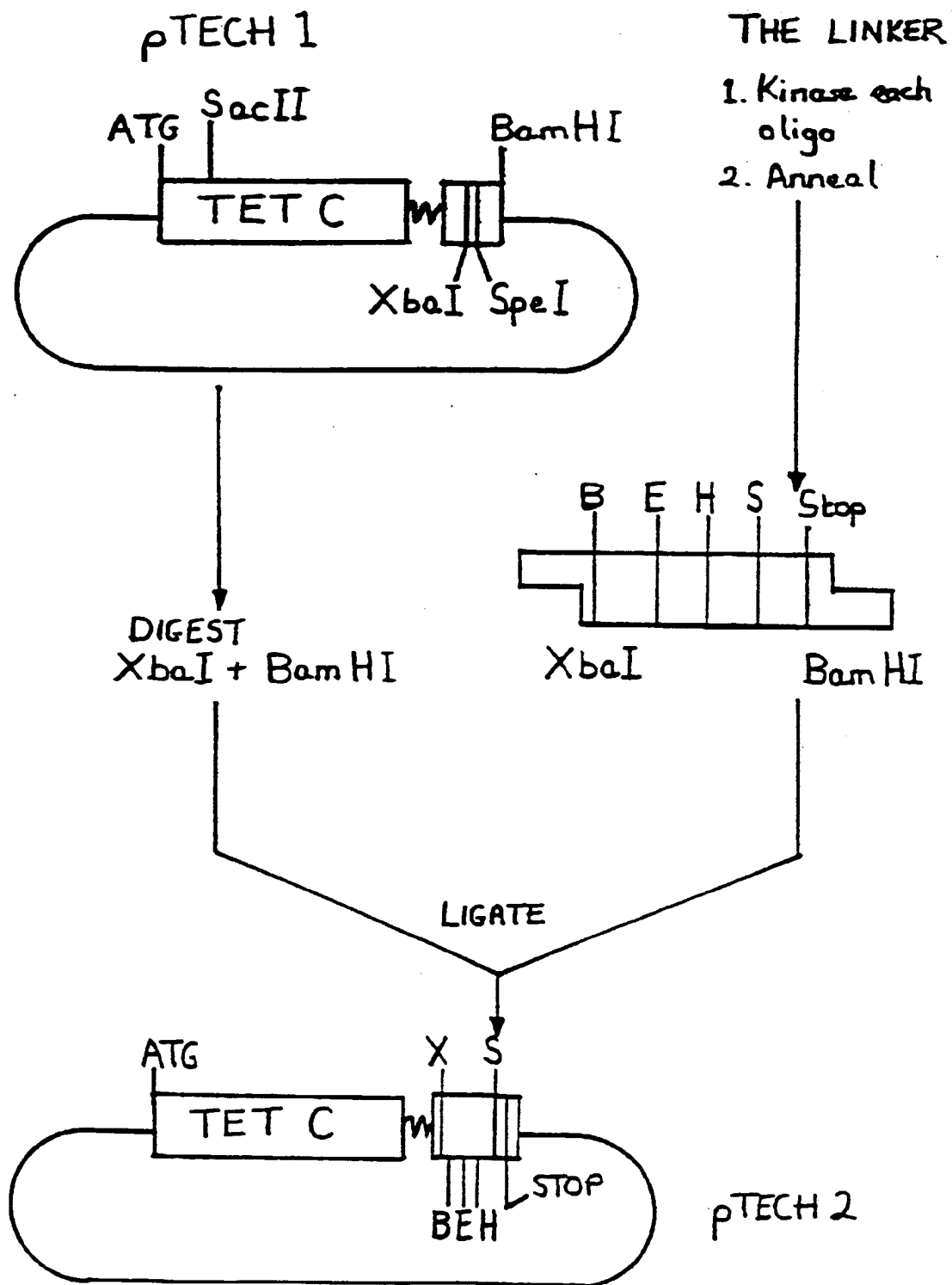


FIGURE 2

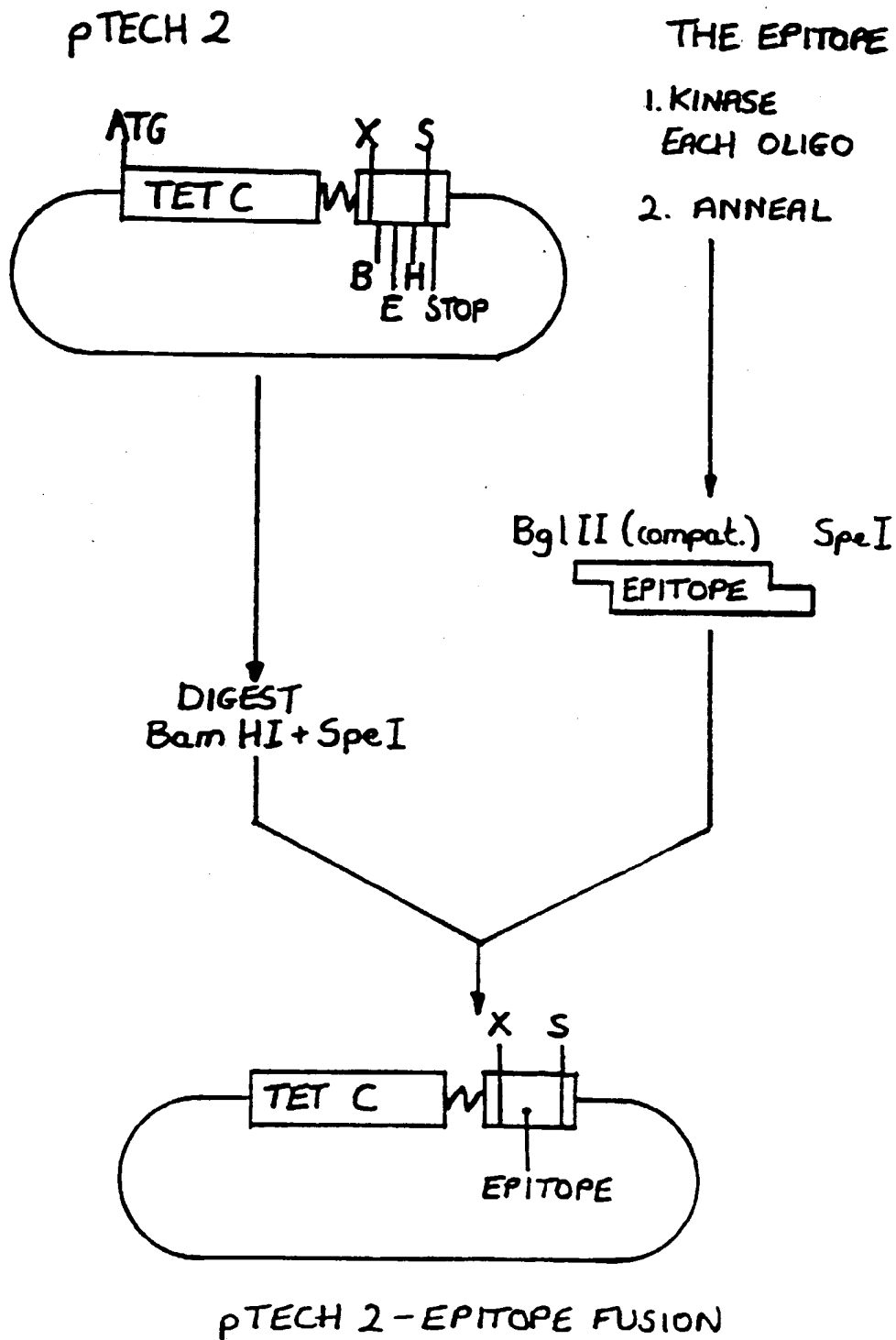


FIGURE 3

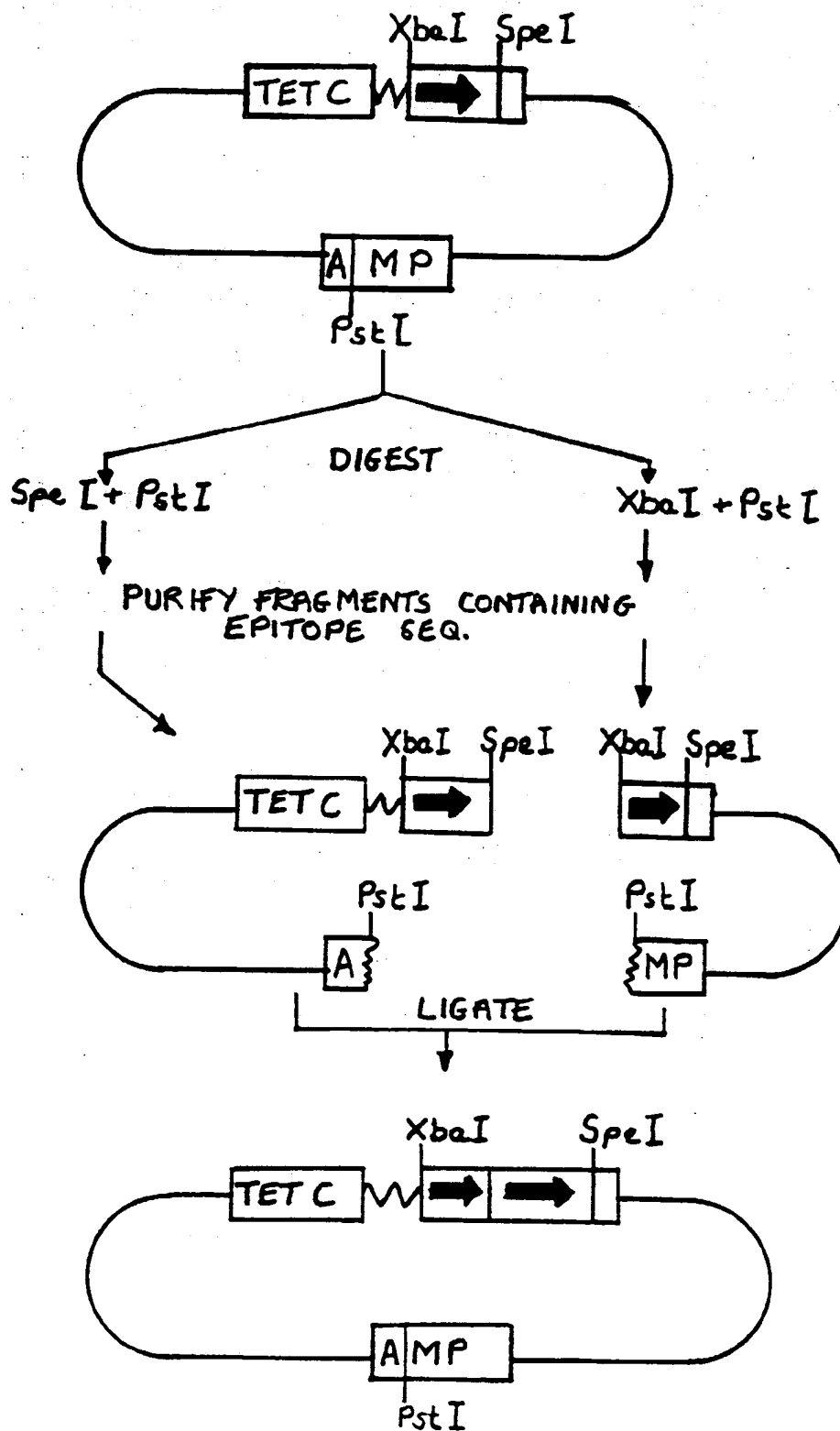


FIGURE 4

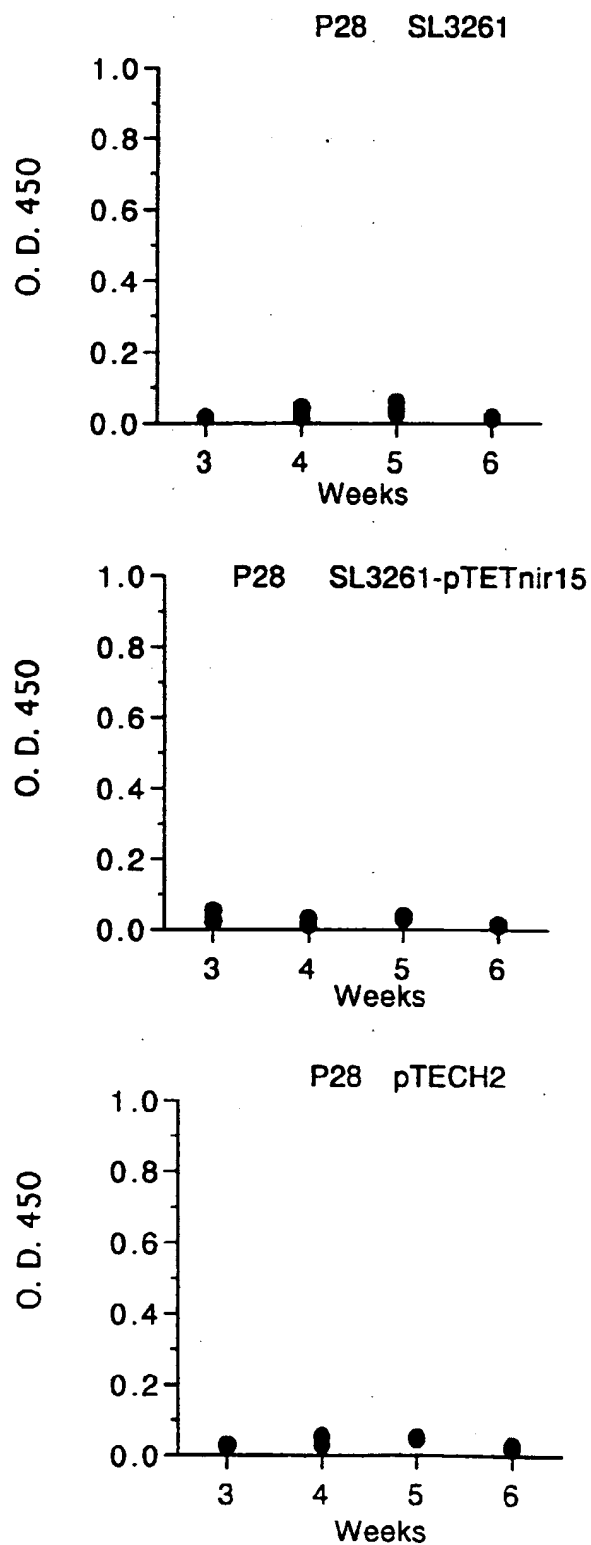


Figure 5

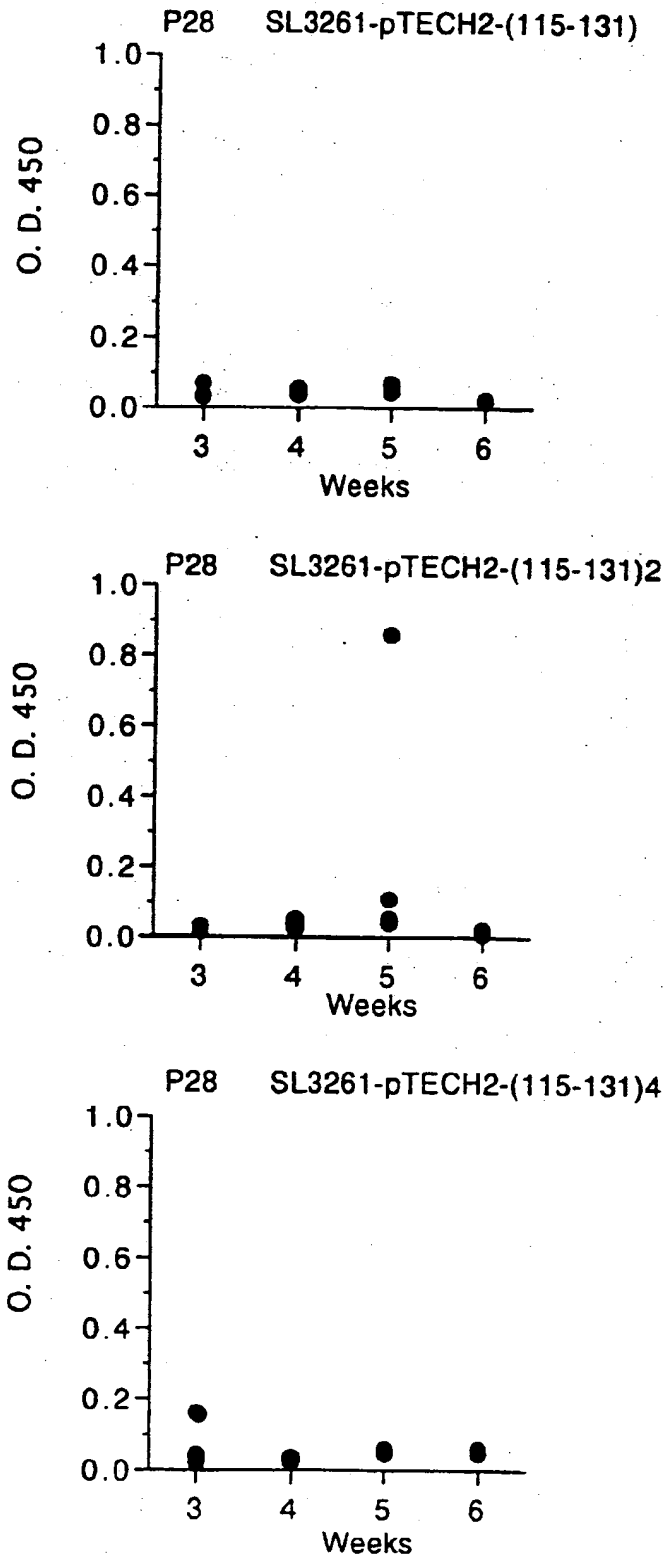


Figure 5 continued

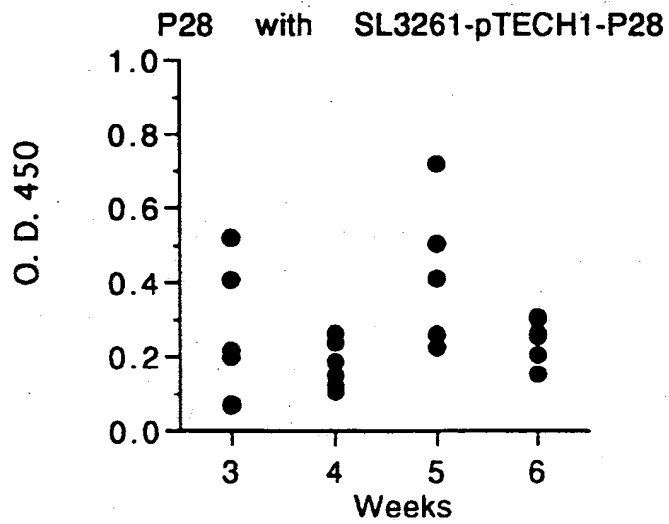
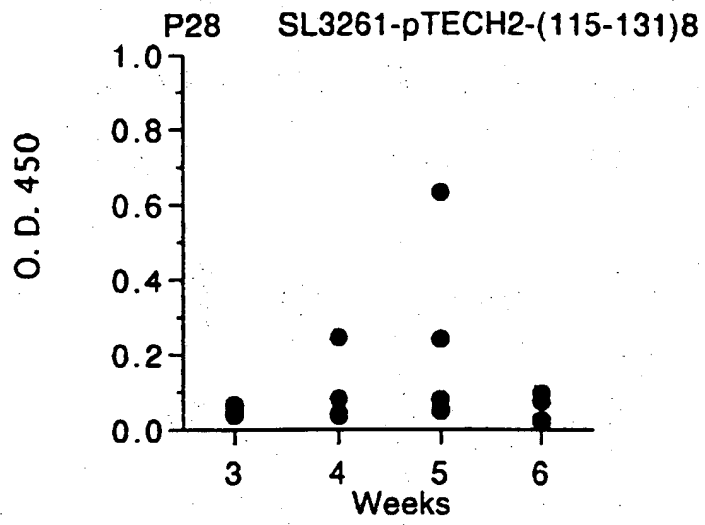


Figure 5 continued

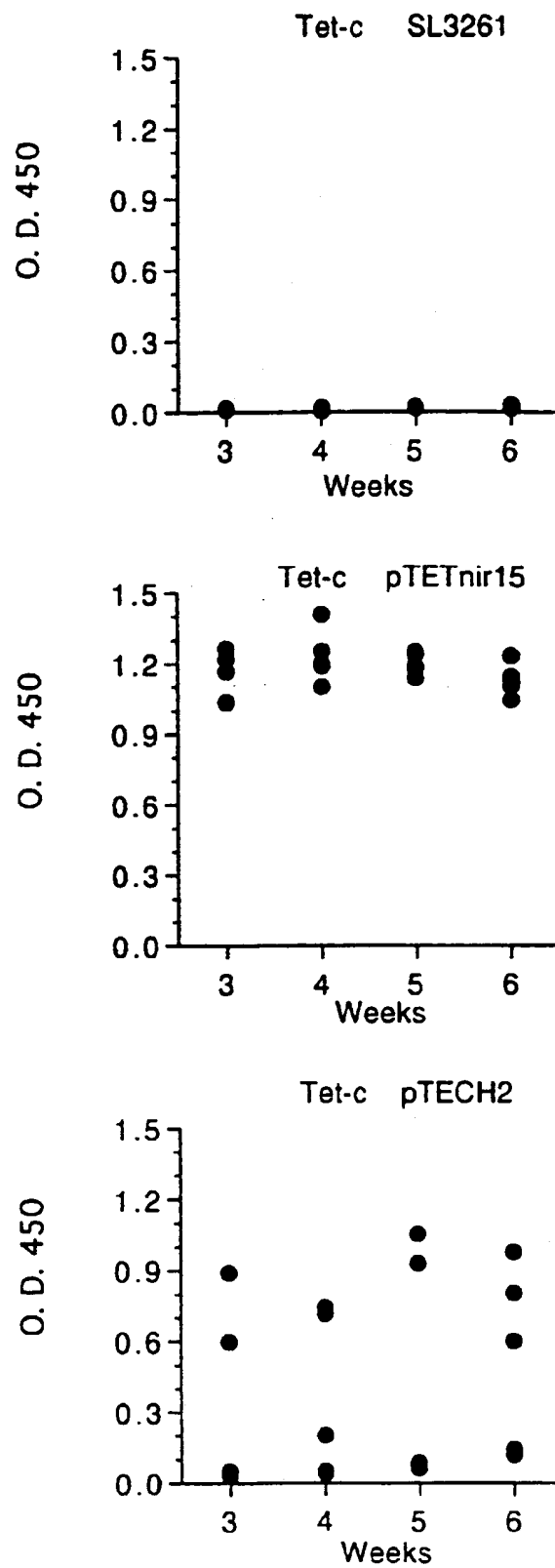


Figure 6

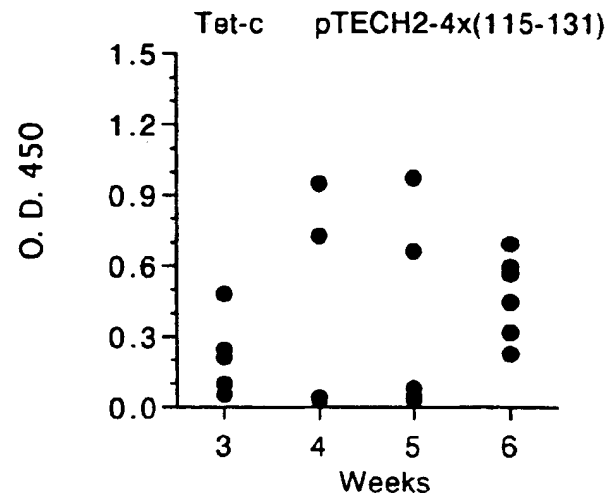
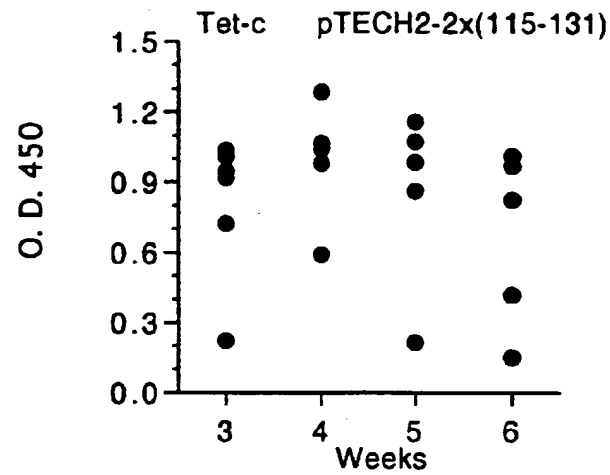
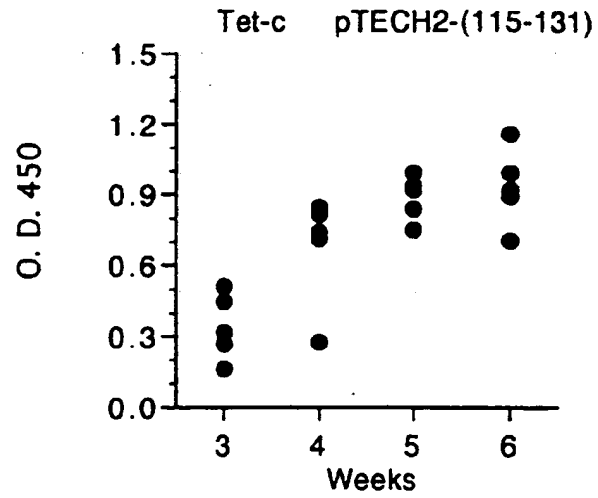


Figure 6 continued

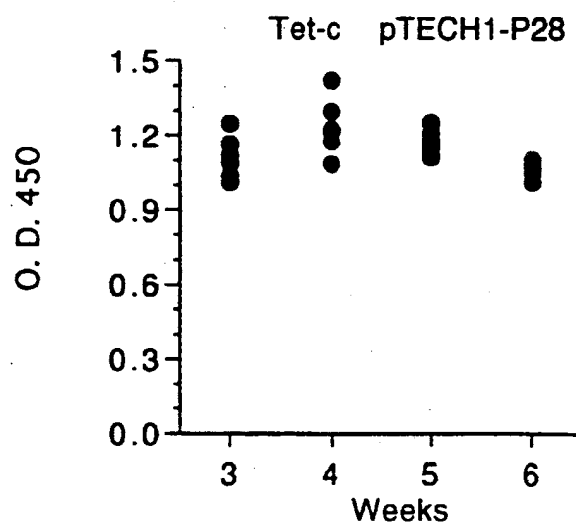
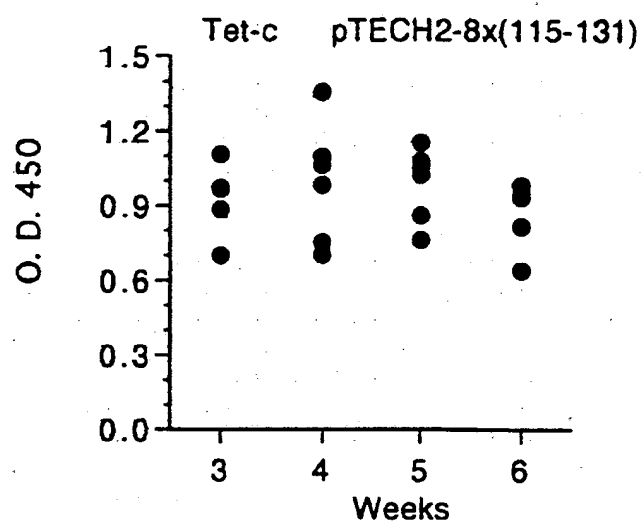


Figure 6 continued

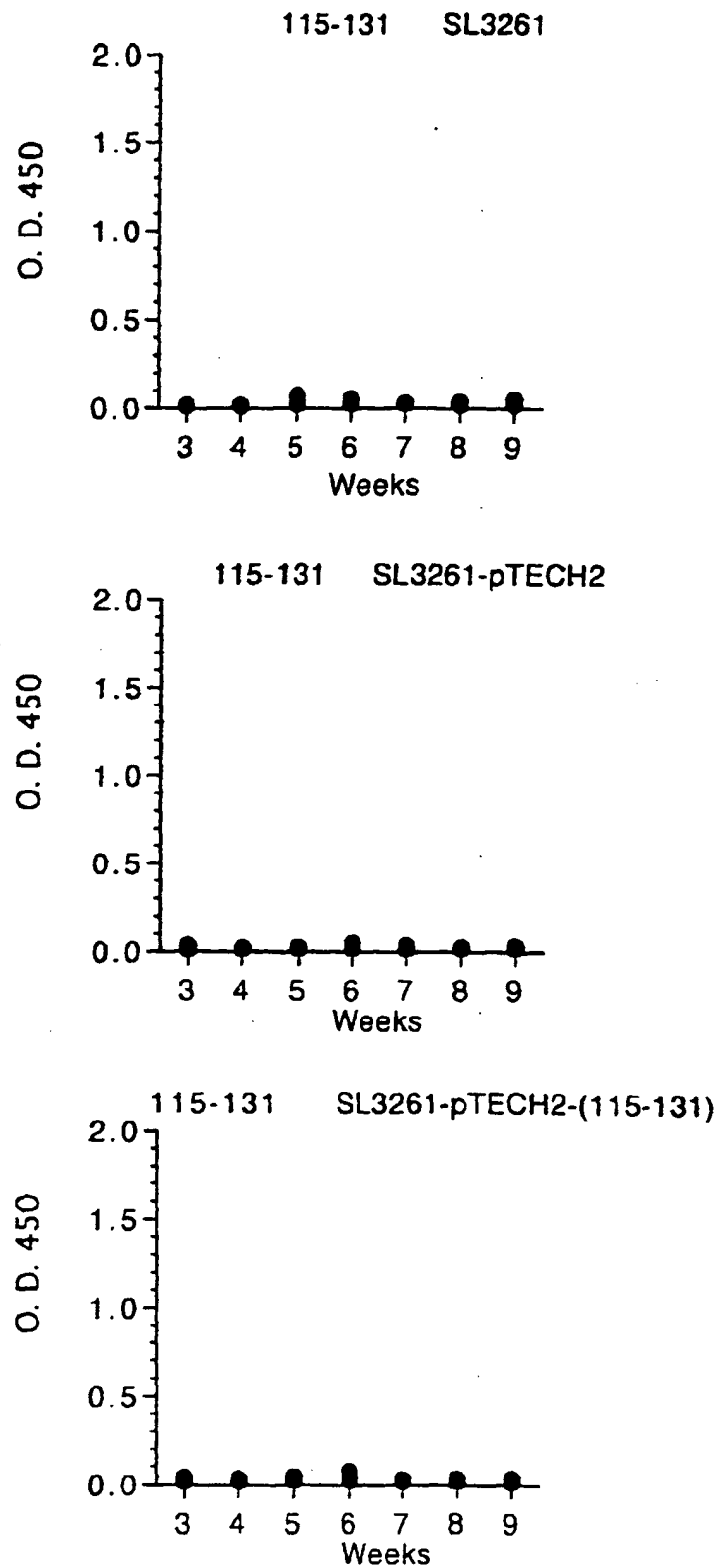


Figure 7

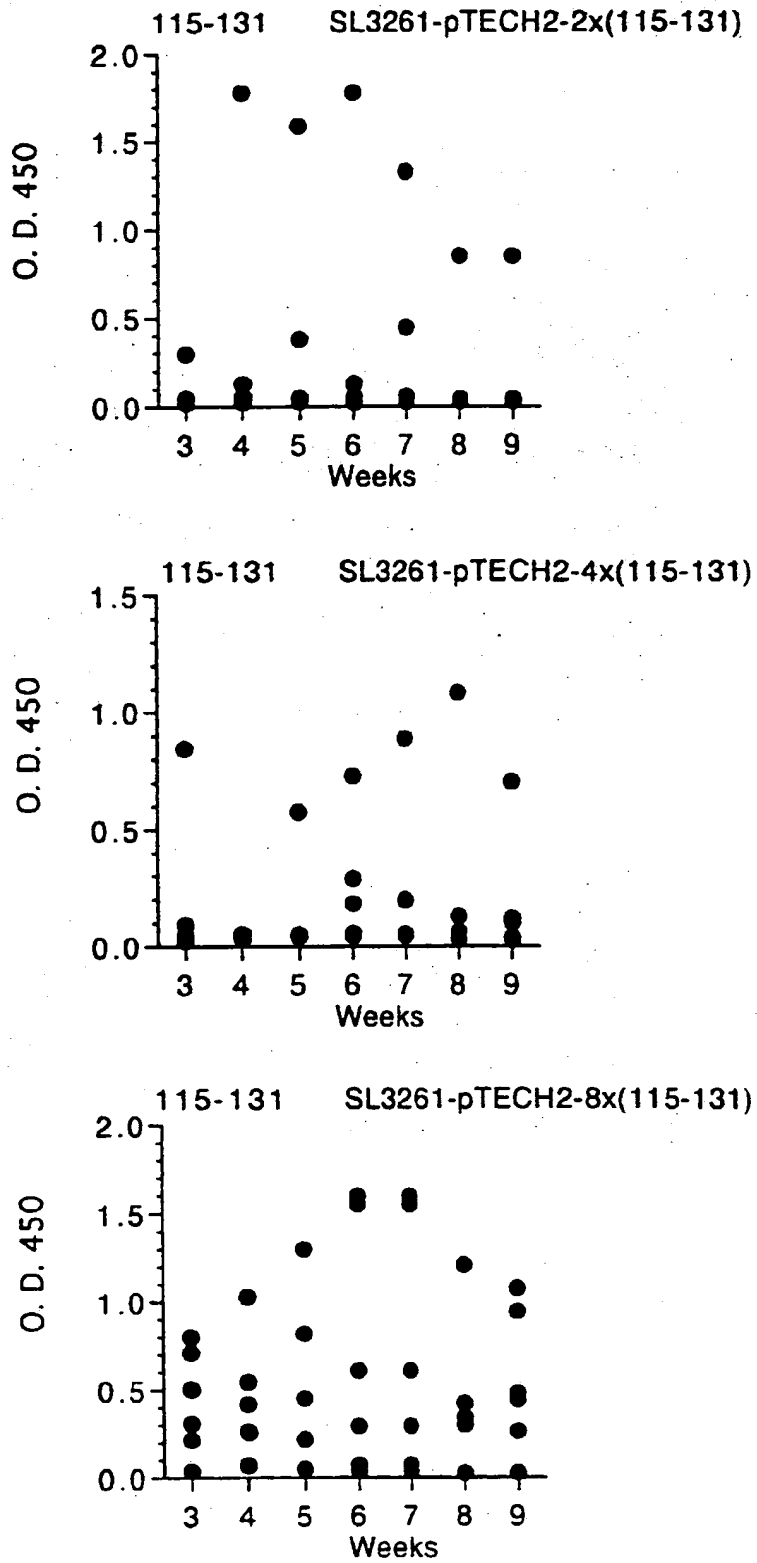


Figure 7 continued

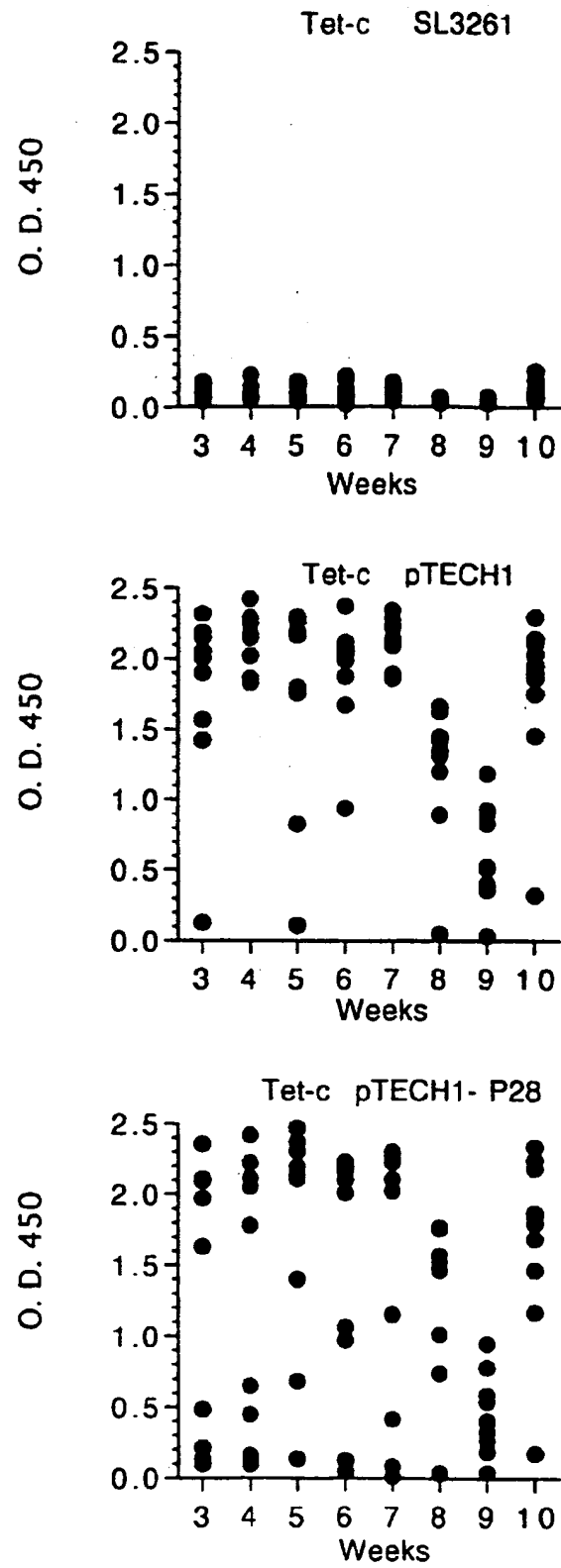


Figure 8

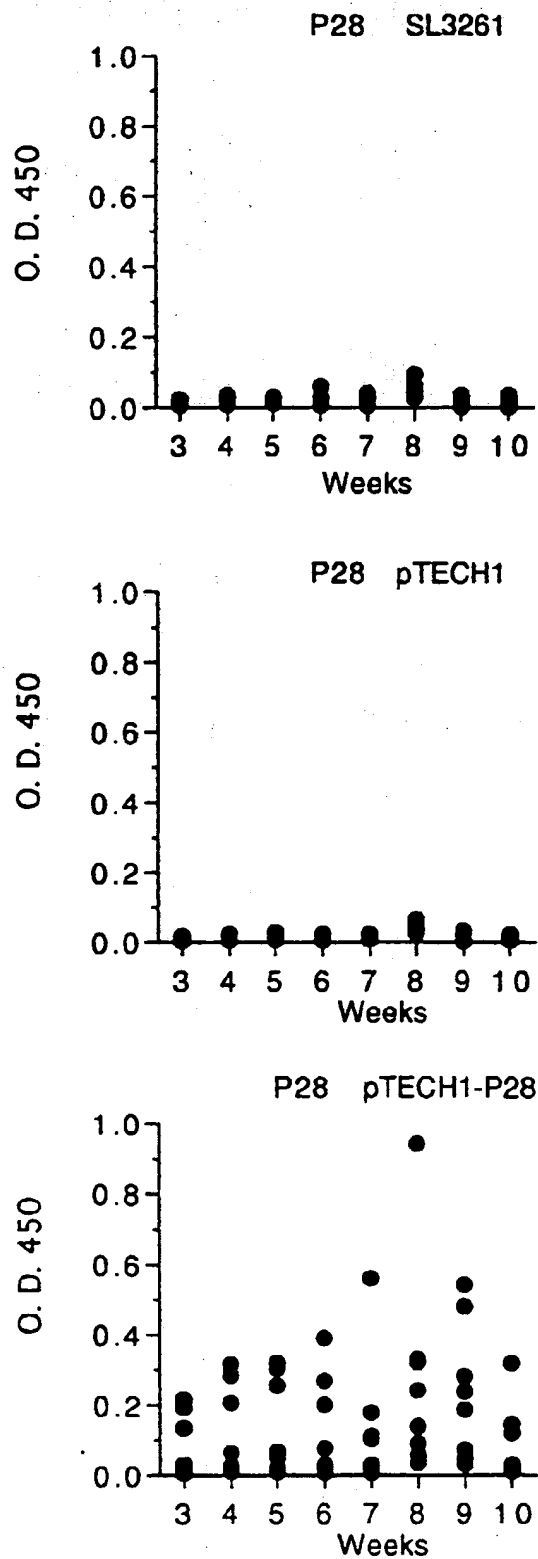


Figure 9

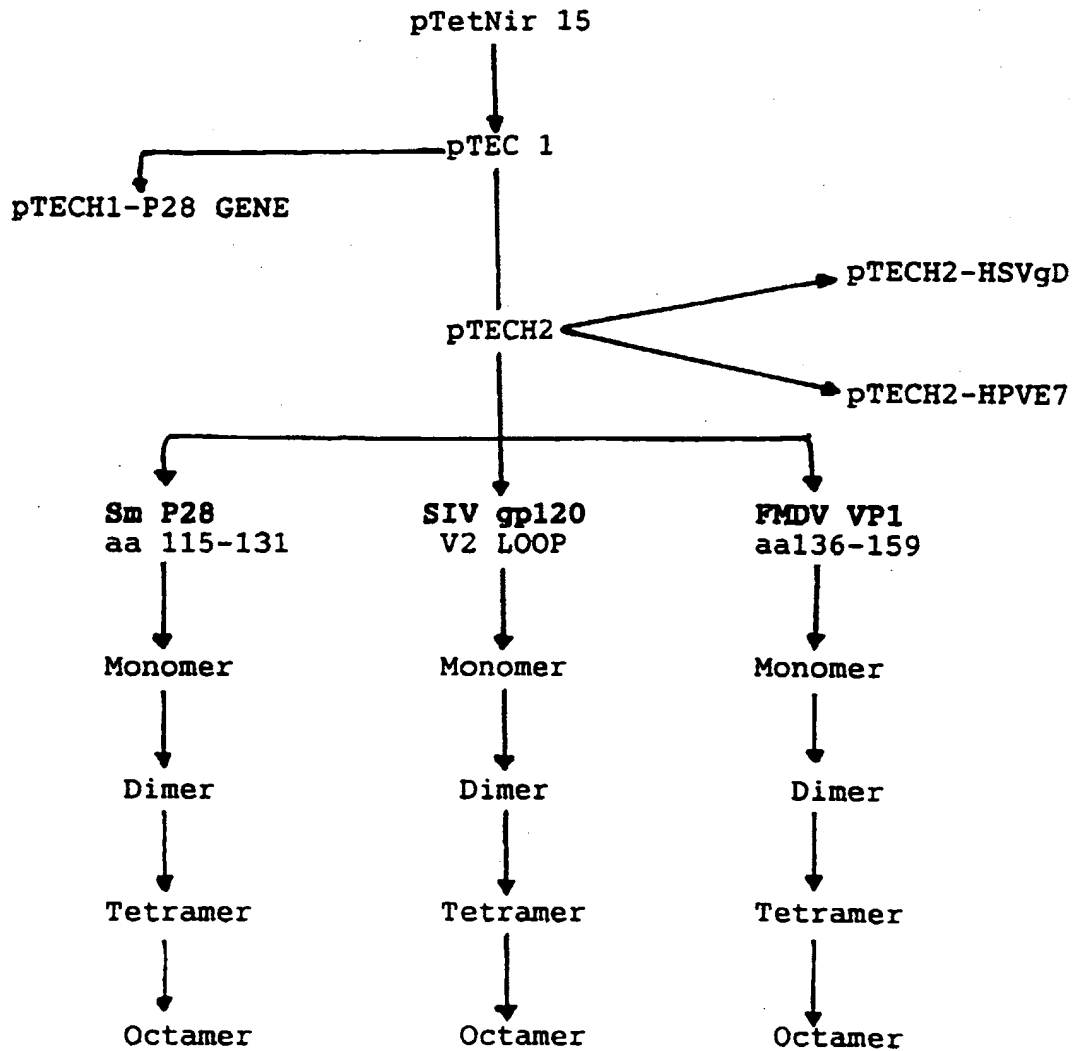
THE CONSTRUCTS

FIGURE 10

Examples of Heteromers



● = *S. mansoni* P28 epitope

▲ = SIV gp 120 V2 epitope

W = Hinge

FIGURE 11

FIGURE 12

DNA Sequence of the Vector pTECH1

(SEQ ID NO: 17)

1bp -TTCAGGTA AATTGATGTACATCAAATGGTACCCCTTGCTGAATCGTTAAGGTAGGCGGT - 60bp

AGGGCCAGATCTTAATCATCCACAGGAGACTTCTGATGAAAAACCTTGATTGTTGGGT
CGACAACGAAGAAGACATCGATGTTATCCTGAAAAAGTCTACCATCTCTGAACCTTGGACAT
CAACAACGATATTATCTCCGACATCTCTGGTTTCAACTCCTCTGTTATCATATATCCAGA
TGCTCAATTGGTGC CGGGCATCAACGGCAAAGCTATCCACCTGGTTAACAACGAATCTTC
TGAAGTTATCGTGCACAAGGCCATGGACATCGAATACAACGACATGTTCAACAACCTTCAC
CGTTAGCTTCTGGCTGCGCGTTCCGAAAGTTTCTGCTTCCACCTGGAACAGTACGGCAC
TAACGAGTACTCCATCATCAGCTCTATGAAGAAACACTCCCTGTCCATCGGCTCTGGTTG
GTCTGTTTCCCTGAAGGGTAACAACCTGATCTGGACTCTGAAAGACTCCGCGGGCGAAGT
TCGTCAGATCACTTTCCGCGACCTGCGGACAAGTTCAACGCGTACCTGGCTAACAAATG
GGTTTTCATCACTATCACTAACGATCGTCTGTCTTCTGCTAACCTGTACATCAACGGCGT
TCGATGGGCTCCGCTGA AATCACTGGTCTGGGCGCTATCCGTGAGGACAACAACATCAC
TCTTAAGCTGGACCGTTGCAACAACAACAACCACTACGTATCCATCGACAAGTTCCGTAT
CTTCTGCAAAGCACTGAACCCGAAAGAGATCGAAAACTGTATACCAGCTACCTGTCTAT
CACCTTCTCGTGACTTCTGGGGTAACCCGCTGCGTTACGACACCGAATATTACCTGAT
CCCGGTAGCTTCTAGCTCTAAAGACGTTTACGCTGAAAAACATCACTGACTACATGTACCT
GACCAACGCGCGCTCTACACTAACGGTAAACTGAACATCTACTACCGACGTCGTACAA
CGGCTGAAATTTCATCATCAAACGCTACACTCCGAACAACGAAATCGATTCTTTGGTTAA
ATCTGGTGACTTCATCAAACCTGTACGTTTCTTCAACAACAACGAACACATCGTTGGTTA
CCCGAAAGACGGTAACGCTTTCAACAACCTGGACAGAATTCTGCGTGTGGTTACAACGC
TCCGGGTATCCCGCTGTACAAAAAATGGAAGCTGTAAACTGCGTGACCTGAAAAACCTA
CTCTGTTACGCTGAAACTGTACGACGACAAAAACGCTTCTCTGGGTCTGGTTGGTACCCA
CAACGGTCAGATCGGTAACGACCCGAACCGTGACATCCGTGATCGCTTCTAACTGGTACTT
CAACCACCTGAAAGACAAAATCCTGGGTTGCGACTGGTACTTCGTTCCGACCGATGAAGG
TTGGACCAACGACGGGCGGGGCCCTCTAGAATCACTAGTTAAGGATCCGCTAGCCCGCC

pTECH1 DNA Sequence continued

TAATGAGCGGGCTTTTTTCTCGGGCAGCGTTGGGTCTGGCCACGGGTGCGCATGATC
GTGCTCCTGTCTGTTGAGGACCGGCTAGGCTGGCGGGGTGCCCTTACTGGTTAGCAGAAT
GAATCACCGATACGCGAGCGAACGTGAAGCGACTGCTGCTGCAAAACGTCTGCGACCTGA
GCAACAACATGAATGGTCTTCGGTTTCGTGTTTCGTAAAGTCTGGAAACGCGGAAGTCA
GCGCTCTTCGGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCTGCTCGGCTGCGGCGAGC
GGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGG
AAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCT
GGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCA
GAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCT
CGTGGCTCTCCTGTTCGACCCCTGCGCTTACCGGATACCTGTCCGCTTTCTCCCTTC
GGGAAGCGTGGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCCGTGTAGGTGCT
TCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTTCAGCCCGACCGCTGCGCCTTATC
CGGTAACATATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGC
CACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTG
GTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCC
AGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCACCGCTGGTAG
CGGTGGTTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGA
TCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACCTACGTTAAGGGAT
TTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAG
TTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAAT
CAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTGGTTTCATCCATAGTTGCCTGACTCCC
CGTGGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGAT
ACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCGCCAGCCGGAAG
GGCCGAGCGCAGAAAGTGGTCTGCAACTTTATCGCCTCCATCCAGTCTATTAAATGTGTG

pTECH1 DNA Sequence continued

CCGGGAAGCTAGAGTAAGTAGTTCCGCCAGTTAATAGTTTTCGCAACGTTGTTGCCATTGC
TGCAGGCATCGTGGTGTACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCA
ACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGG
TCCTCCGATCGTTGTGAGAAGTAAGTTGGCCGCGAGTGTATCACTCATGGTTATGGCAGC
ACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTA
CTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTCCTTTGCCCGGCGTC
AACACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACG
TTCTTCGGGGCGAAAACCTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTGATGTAACC
CACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTTACCAGCGTTTCTGGGTGAGC
AAAAACAGGAAGGCAAAATGCGCAAAAAAGGAATAAGGGCGACACGGAAATGTTGAAT
ACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAG
CGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCC
CCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACTATAAAAA
TAGGCGTATCACGAGGCCCTTTTCGTCTTCAAGAA - 3754bp

FIGURE 13

DNA Sequence of the Vector pTECH2

(SEQ ID NO: 18)

1bp - TTCAGGTAAATTTGATGTACATCAATGGTACCCCTTGCTGAATCGTTAAGGTAGGCGGT - 60bp

AGGGCCCAGATCTTAATCATCCACAGGAGACTTTTCGATGAAAAACCTTGATTGTTGGT

CGACAACGAAGAAGACATCGATGTTATCCTGAAAAAGTCTACCATTCGAACTTGGACAT

CAACAACGATATTATCTCCGACATCTCTGGTTTCAACTCCTCTGTTATCACAATATCCAGA

TGCTCAATTGGTCCGGGCATCAACGGCAAGCTATCCACCTGGTTAACAACGAATCTTC

TGAAGTTATCTGTCACAAGGCCATGGACATCGAATACAACGACATGTTCAACAACCTTCAC

CGTTAGCTTCTGGCTCGCGCTTCGAAAGTTTCTGCTTCCACCTGGAAACAGTACGGCAC

TAACGAGTACTCCATCATCAGCTCTATGAAGAAACACTCCCTGTCCATCGGCTCTGGTTG

GTCTGTTTCCCTGAAGGGTAAACAACCTGATCTGGACTCTGAAAGACTCCGCGGGCGAAGT

TCGTCAAGTCACTTTCCGGCAGCTGCCGGACAAGTTCAACGGCTACCTGGCTAACAAATG

GGTTTTCACTACTATCACTAACGATCGTCTGTCTTCTGCTAACCTGTACATCAACGGCGT

TCTGATGGGCTCCGCTGAAATCACTGGTCTGGGCGCTATCCGTGAGGACAACAACATCAC

TCTTAAGCTGGACCGTTGCAACAACAACAACAGTACGTATCCATCGACAAGTTCCGTAT

CTTCTGCAAGCACTGAACCCGAAAGAGATCGAAAACTGTATACCAGCTACCTGTCTAT

CACCTTCCTGCGTGACTTCTGGGGTAACCCGCTGCGTTACGACACCGAATATTACCTGAT

CCCGGTAGCTTCTAGCTCTAAAGACGTTCACTGAAAAACATCACTGACTACATGTACCT

GACCAACGCGCGCTCTACACTAACGGTAACTGAACATCTACTACCGACGTTCTGTACAA

CGGCTTGAAATTCATCATCAAAACGCTACACTCCGAACAACGAANTCGATTCTTTCTGTTAA

ATCTGGTGACTTCACTCAAACTGTACGTTTCTTACAACAACAACGAACACATCGTTGGTTA

CCCGAAAGACGGTAACGCTTTCAACAACCTGGACAGAAATCTGCGTGTGGTTACAAAGC

TCCGGGTATCCCGCTGTACAAAAAATGGAAGCTGTTAACTGCGTGACCTGAAAAACCTA

CTCTGTTCACTGAACTGTACGACGACAAAAACGCTTCTCTGGGTCTGGTTGGTACCCA

CAACGGTCAGATCGGTAACGACCCGAACCGTGACATCTGTATCGCTTCTAACTGGTACTT

CAACCACCTGAAAGACAAAATCCTGGGTTGCGACTGGTACTTGGTTCCGACCGATGAAGG

TTGACCAACGACGGGCTGGGGCCCTCTAGAGGATCCGATATCAAGCTTACTAGTTAATG

ATCCGCTAGCCCGCTAATGAGCGGGCTTTTTTTCTCGGGCACCGTTGGGTCTCGGCA

CGGGTGGCATGATCGTGTCTCTGTCTGTAGGACCCGGCTAGGCTGGCGGGGTGCGCTT

pTECH2 DNA Sequence continued

ACTGGTTAGCAGAATGAATCACCGATACGCGAGCGAACGTGAAGCGACTGCTGCTGCAAA
 ACGTCTGCGACCTGAGCAACAACATGAATGGTCTTCGGTTTCCGTGTTTCGTAAAGTCTG
 GAAACGCGGAAGTCAGCGCTCTTCGGCTTCCTCGCTCACTGACTCGCTCGGCTCGGTGCT
 TCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATC
 AGGGGATAACGCAGGAAGAACAATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAA
 AAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAA
 TCGACGCTCAAGTCAGAGGTGGCGAAACCGACAGGACTATAAAGATACCAGGCGTTTCC
 CCTGGAAGCTCCCTCGTGGCTCTCCGTTCGACCCCTGCGGCTTACCGGATACCTGTC
 CGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAG
 TTCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGA
 CCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATC
 GCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTAC
 AGAGTTCCTGAAGTGGTGGCCTAACTACGGCTACCTAGAAGGACAGTATTTGGTATCTG
 CGCTCTGCTGAAGOCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAACA
 AACCACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCCGAGAAAAA
 AGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAA
 CTCACGTTAAGGGATTTTGGTCAAGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTT
 AATTTAAAAATGAAGTTTTTAAATCAATCTAAAGTATATAGTAAACTTGGTCTGACAG
 TTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTGCTTCATCCAT
 AGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCC
 CAGTCTGCAATGATACCGCGAGACCCACGCTCACGGGCTCCAGATTTATCAGCAATAAA
 CCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCTGCAACTTTATCCGCTCCATCCA
 GTCTATTAAATGTTGCGGGAAGCTAGAGTAAGTAGTTCCGCAGTTAATAGTTTGGCGAA
 CGTTGTTGCCATGCTGCGGCATCGTGGTGTACGCTCGTCTTGGTATGGCTTCATT
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 GGTAGCTCCTTCGGTCTCCGATCGTTGTGAGAAGTAAGTTGGCCGAGTGTATCACT
 CATGGTTATGGCAGCACTGCATAATTCTCTTACTGTGTCATGCCATCCGTAAGATGCTTTTC

pTECH2 DNA Sequence continued

TGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGATGCGGCGACCGAGTTG
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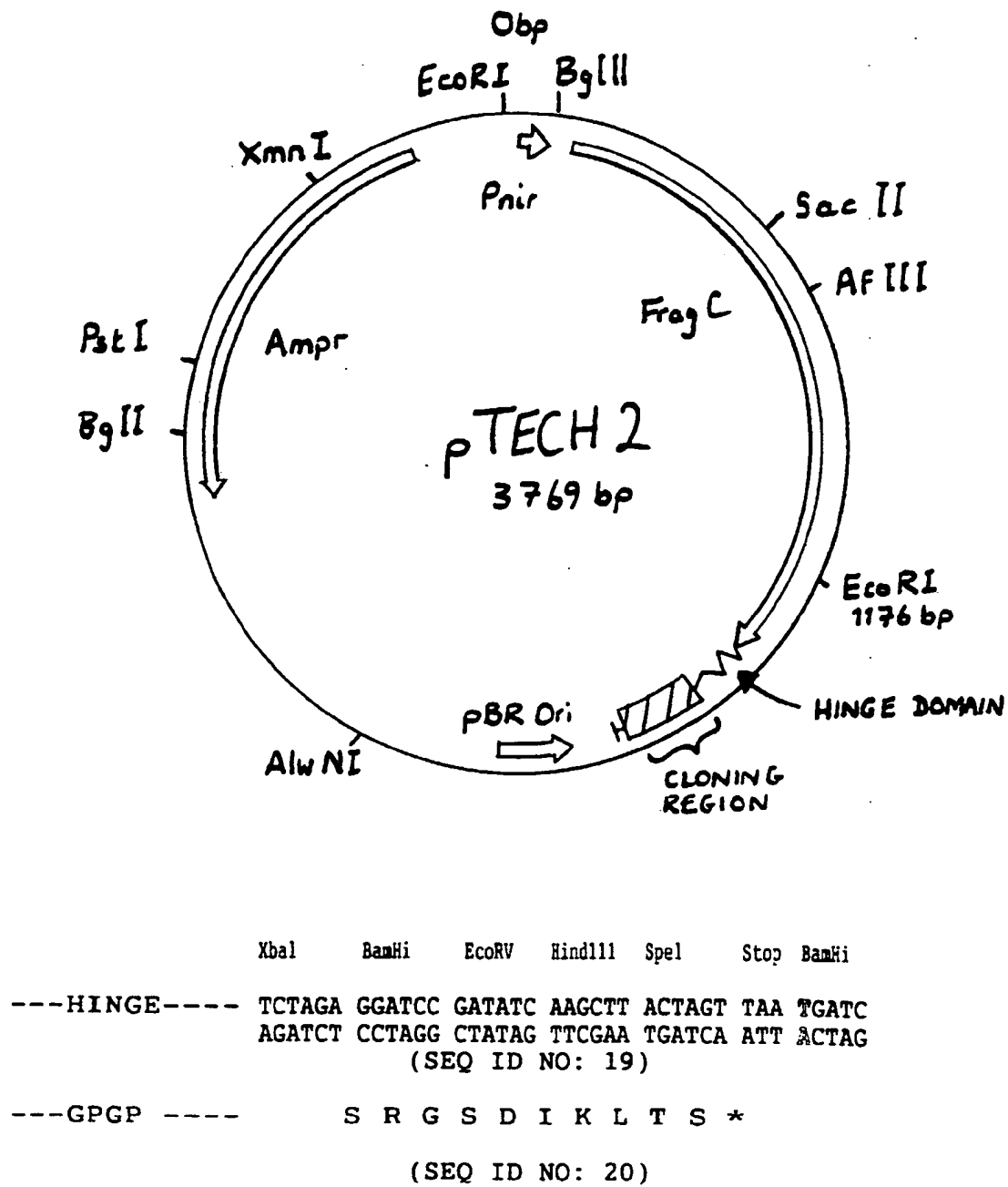


FIGURE 14